

[illegible]

Fig. 1A

G N N P D Y W K Y G E A A S T E C N S V 191
 GGA AAC AAT CCT GAT TAC TGG AAG TAC TGG GAG GCA GCC AGT ACC GAA TGC AAC AGC GTC 606

 C F G D H T Q P C G G D G R I I L F D T 211
 TGC TTC GGG GAT CAC ACC CAA CCC TGT GGT GGC GAT GGC AGG ATC ATC CTC TTT GAT ACT 666

 L V G A C G G N Y S A M S S V Y S P D 231
 CTC GTG GGC GCC TGC GGT GGC AAC TAC TCA GCC ATG TCT TCT GTG GTC TAT TCC CCT GAC 726

 F P D T Y A T G R V C Y W T I R V P G A 251
 TTC CCC GAC ACC TAT GCC ACG GGC AGG GTC TGC TAC TGG ACC ATC CGG GTT CCG GGG GCC 786

 S H I H F S F P L F D I R D S A D M V E 271
 TCC CAC ATC CAC TTC AGC TTC CCC CTA TTT GAC ATC AGG GAC TCG GCG GAC ATG GTG GAG 846

 L L D G Y T H R V L A R F H G R S R P P 291
 CTT CTG GAT GGC TAC ACC CAC CGT GTC CTA GCC CGC TTC CAC GGG AGG AGC CGC CCA CCT 906

 L S F N V S L D F V I L Y F F S D R I N 311
 CTG TCC TTC AAC GTC TCT CTG GAC TTC GTC ATC TTG TAT TTC TTC TCT TCT GAT CGC ATC AAT 966

 Q A Q G F A V L Y Q A V K E E L P Q E R 331
 CAG GCC CAG GGA TTT GCT GCT TTA TAC CAA GCC GTC AAG GAA GAA CTG CCA CAG GAG AGG 1026

2/95

Fig. 1B

P A V N Q T V A E V I T E Q A N L S V S	351
CCC GCT GTC AAC CAG ACG GTG GCC GAG GTG ATC ACG GAG CAG GCC AAC CTC AGT GTC AGC	1086
A A R S S K V L Y V I T T S P S H P P Q	371
GCT GCC CGG TCC TCC AAA GTC CTC TAT GTC ATC ACC ACC AGC CCC AGC CAC CCA CCT CAG	1146
T V P G S N S W A P P M G A G S H R V E	391
ACT GTC CCA GGT AGC AAT TCC TGG GCG CCA CCC ATG GGG GCT GGA AGC CAC AGA GTT GAA	1206
G W T V Y G L A T L L I L T V T A I V A	411
GGA TGG ACA GTC TAT GGT CTG GCA ACT CTC CTC ATC ACA GTC ACA GCC ATT GTA GCA	1266
K I L L H V T F K S H R V P A S G D L R	431
AAG ATA CTT CTG CAC GTC ACA TTC AAA TCC CAT CGT GTT CCT GCT TCA GGG GAC CTT AGG	1326
D C H Q P G T S G E I W S I F Y K P S T	451
GAT TGT CAT CAA CCA GGG ACT TCG GGG GAA ATC TGG AGC ATT TTT TAC AAG CCT TCC ACT	1386
S I S I F K K K L K G Q S Q Q D D R N P	471
TCA ATT TCC ATC TTT AAG AAG AAA CTC AAG GGT CAG AGT CAA CAA GAT GAC CGC AAT CCC	1446
L V S D *	
CTT GTG AGT GAC TAA	

3 / 95

Fig. 1C

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476
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AAACCCACTGTGCCTAGGACTTGAGGTCCCTCTTTGAGCTCAAGGCTGCCGTGGTCAACCTCTCCTGTGTTCTCTC 1540
TGACAGACTCTTCCCTCTCTCCCTCTGCCCTCGGCCTCTTTCCGGGAAACCCCTCCTCTACAGACTAGGAAGAGGCACCT 1620
GCTGCCAGGGCAGGCAGAGCCTGGATTCTCTCCTGCTT 1657

Fig. 1D

GTCGACCCACGGTCCGCCGGCTCCCGGTGCTGCCCCCTCTGCCCCGGCGCCGGGTCCCGCACTGACGGCC 79

M A P A P A A R L A L L S A A A L T L A 19
C ATG GCG CCG CCC GCC GCC CGT CTC GCG CTG CTC TCC GCC GCT GCG CTC ACT CTG GCG 137

A R P A P G P R S G P E C F T A N G A D 39
GCC CGG CCC GCG CCC GGT CCC CGC TCC GGC CCC GAG TGC TTC ACA GCC AAC GGT GCA GAT 197

Y R G T Q S W T A L Q G G K P C L F W N 59
TAC AGG GGA ACA CAG AGC TGG ACA GCG CTG CAA GGT GGG AAG CCA TGT CTG TTC TGG AAC 257

E T F Q H P Y N T L K Y P N G E G L G 79
GAG ACT TTC CAG CAT CCG TAC AAC ACG CTG AAG TAC CCC AAC GGG GAA GGA GGA CTG GGC 317

E H N Y C R N P D G D V S P W C Y V A E 99
GAG CAC AAT TAT TGC AGA AAT CCA GAT GGA GAC GTG AGC CCT TGG TGC TAC GTG GCC GAG 377

Fig. 1E

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5/95

H	E	D	G	G	V	Y	W	K	Y	C	E	I	P	A	C	Q	M	P	G	N	119
CAT	GAG	GAC	GGA	GTC	TAC	TGG	AAG	TAC	TGT	GAA	ATT	CCT	GCC	TGC	CAG	ATG	CCT	GGA	AAC	437	
L	G	C	Y	K	D	H	G	N	P	P	P	L	T	G	T	S	K	T	S	139	
CTT	GGC	TGC	TAC	AAG	GAT	CAT	GGA	AAC	CCA	CCT	CCT	CTC	ACG	GGC	ACC	AGT	AAA	ACC	TCT	497	
N	K	L	T	I	Q	T	C	I	S	F	C	R	S	Q	R	F	K	F	A	159	
AAC	AAG	CTC	ACC	ATA	CAA	ACC	TGT	ATC	AGC	TTC	TGT	CGG	AGT	CAG	AGA	TTC	AAG	TTT	GCT	557	
G	M	E	S	G	Y	A	C	F	C	G	N	P	D	Y	W	K	H	G	179		
GGG	ATG	GAG	TCA	GGC	TAT	GCC	TGC	TTC	TGT	GGG	AAC	AAT	CCT	GAC	TAC	TGG	AAG	CAC	GGG	617	
E	A	A	S	T	E	C	N	S	V	C	F	G	D	H	T	Q	P	C	G	199	
GAG	GCG	GCC	AGC	ACC	GAG	TGC	AAT	AGT	GTC	TGC	TTC	GGG	GAC	CAC	ACG	CAG	CCC	TGC	GGT	677	
G	D	G	R	I	I	L	F	D	T	L	V	G	A	C	G	G	N	Y	S	219	
GGG	GAC	GGC	AGG	ATT	ATC	CTC	TTT	GAC	ACT	CTC	GTG	GGC	GCC	TGC	GGT	GGG	AAC	TAC	TCA	737	
A	M	A	A	V	V	Y	S	P	D	F	P	D	T	Y	A	T	G	R	V	239	
GCC	ATG	GCA	GCC	GTG	GTG	TAC	TCC	CCT	GAC	TTC	CCT	GAC	ACC	TAC	GCC	ACT	GGC	AGA	GTC	797	
C	Y	W	T	I	R	V	P	G	A	S	R	I	H	F	N	F	T	L	F	259	
TGC	TAC	TGG	ACC	ATC	CGG	GTT	CCA	GGA	GCC	TCT	CGC	ATC	CAT	TTC	AAC	TTC	ACC	CTG	TTT	857	
D	I	R	D	S	A	D	M	V	E	L	L	D	G	Y	T	H	R	V	L	279	
GAT	ATC	AGG	GAC	TCT	GCA	GAC	ATG	GTG	GAG	CTG	CTG	GAC	GGC	TAC	ACC	CAC	CGC	GTC	CTG	917	

Fig. 1F

V R L S G R R S R P P L S F N V S L D F V 299
 GTC CGG CTC AGT GGG AGG AGC CGC CCG CCT CTG TCT TTC AAT GTC TCT CTG GAT TTT GTC 977

 I L Y F F S D R I N Q A Q G F A V L Y Q 319
 ATT TTG TAT TTC TTC TCT TCT GAT CGC ATC AAT CAG GCC CAG GGA TTT GCT GTG TTG TAC CAA 1037

 A T K E E P P Q E R P A V N Q T L A E V 339
 GCC ACC AAG GAG GAA CCG CCA CAG GAG AGA CCT GCT GTC AAC CAG ACC CTG GCA GAG GTG 1097

 I T E Q A N L S V S A A H S S K V L Y V 359
 ATC ACC GAG CAA GCC AAC CTC AGT GTC AGC GCT GCC CAC TCC TCC AAA GTC CTC TAT GTC 1157

 I T P S P S H P P Q T A Q V A I P G H R 379
 ATC ACC CCC AGC CCC AGC CAC CCT CCG CAG ACT GCC CAG GTA GCC ATT CCT GGG CAC CGT 1217

 Q L G P T A T E W K D G L C T A W R P S 399
 CAG TTG GGG CCA ACA GCC ACA GAG TGG AAG GAT GGA CTG TGT ACG GCC TGG CGA CCC TCC 1277

 S S S Q S Q Q L S Q R F F C M S H L N L 419
 TCA TCC TCA CAG TCA CAG CAG TTG TCG CAA AGA TTC TTC TGC ATG TCA CAT TTA AAT CTC 1337

 I E S L H Q E T L G T V V S L G L L E I 439
 ATC GAG TCC CTG CAT CAG GAG ACC TTA GGG ACT GTC GTC AGC CTG GGG CTT CTG GAG ATA 1397

 S G P F S M N L P L Q S P S L R S S R 459
 TCT GGA CCA TTT TCT ATG AAC CTT CCA CTA CAA TCT CCA TCT TTA AGA AGA AGC TCA AGG 1457

6/95

Fig.1G

V	R	N	K	M	T	A	I	P	S	*	
GTC	AGA	GTC	AAC	AAG	ATG	ACC	GCA	ATC	CCC	TCG	TGA
											471
											1493
GTG	ACT	GAA	GGC	CC	CTG	CAT	GAG	AG	CTC	CG	1572
CCT	GCC	TTCC	CAT	TCA	CC	ATC	CT	TTT	TGG	AG	1651
GTAC	CAG	CC	CTG	CT	GCT	GGG	AT	GGT	TA	AG	1730
CTCT	TGG	GTGG	AG	GTAT	AGT	AG	AT	GGT	TTT	TCT	1809
CCCT	GTCT	TTAC	AG	TTTG	CAAT	AG	AG	CTG	TA	AG	1888
GTGG	CA	TTGG	CC	CTAG	AG	CC	CA	GTG	AG	CT	1967
AGTCC	GAG	GG	ACT	GAG	AG	CC	CA	GTG	AT	CT	2046
GGCA	AG	CC	CTG	AG	AT	TG	TC	CA	TTT	TCT	2125
TAGCC	CT	CA	AG	TA	CTCT	GT	GG	AA	TC	AG	2204
AGCT	GGG	CTG	TA	GC	CTAG	AG	CT	GG	CT	GT	2283
TGGG	CTG	TA	GC	CTAG	AG	CT	GG	CT	GT	AG	2362
GGCT	GT	AG	CT	GG	CT	GT	AG	CT	GG	CT	2441
GACCC	TA	GG	TTCT	AT	CC	AG	CA	CTA	TG	AG	2520
TTCC	TAG	GT	GC	AT	CA	TTT	AA	AG	CA	GT	2599
AGAG	TAG	GT	AG	TA	GG	CT	CT	GG	CT	TA	2678
GATCC	CCC	AG	GA	AA	AG	CT	GC	AG	CT	GC	2757
CTGC	AG	CT	GG	AA	GT	GG	CT	TA	AG	CT	2836
GCCT	CT	GC	CT	GG	TA	CC	CT	TA	AG	CT	2915
TCCT	CT	AG	CT	GG	CT	TA	AG	CT	GG	CT	2994
TGAC	CT	AG	CT	GG	CT	TA	AG	CT	GG	CT	3073
TACAG	GG	GT	TA	CT	CA	TT	TA	CT	GG	AA	3152
CACTA	CA	TA	AG	AA	TA	GA	CT	GA	CA	GG	3231

Fig. 1H

CCCTGAGACCAAGTGTGAGTCACAGAGTGCCATGTGCGTAGTGCCATAAAGGATATGGGTTCTTAACCAGGGAAGGCTC 3310
ATAGCAGGCCAGGACATTTTTCAGCTCAGAGCACTGGCCCCAGGCTTCCTCTAAGCCACCACACTCACCTGTCTCTTCCT 3389
ATCTCGGACACAGGAAGCAAGCCCCAGTGTGTGGCAGCTGCGGCTCAGCATTTGGTGTCCTCCAGGAAGGCGGTGGATG 3468
TGCCCCAGCTCCTTTTGTGTGGGCTGCGACAGCCCAACACTGCAGGGCCACCTTCTCTCTTGGGGGTAGGGACAC 3547
ATAAGGAAAACATAACCCACCTCCAACACAGACAGAGGACAGTGGGAAGGAAGGGCTGTAAATCACCCAGGCCAGACCTC 3626
CAGAAATGACAGGCACAGTCTGTTAGAACCTGTAGGCAGCCAGTCACAGAGGGCCTTTGTGCTGTTAACAACCTTGCCCTG 3705
GAGCATAGGGGTAAGCCGAGGAGAGAGCAGCCCTCAGAGACATCAGCTAAAAACATAGTGCCCCCTATGTCCCTCCCT 3784
TCCTGTCACACTGCTTACAAAGCAGAGACAGAGTAGGAAGAGGCTTTCATCCTCTCCACATCAGCAAGGATAGGGCT 3863
GCGGCTGCCATAAGTGAGCAAGGAGAACAGAGCTCTGGACTTCTCTAAATGTGGGCTCTGGCTTCAGACTCCTCAGCCA 3942
AAAGCTCTTGAAGATCAAAGCTCTGGCGGTACAGCTGTCCCTGGCCTGTGGGCCAGCCCCATGGGATGTGCCCTGGGCCAG 4021
GTGCCACCCACGGCTCACTGTCAATCCAGGAGGACCCACCTGATGCTCCTCATCATCCGCTGGCCTGACACTATCA 4100
GAGCTCGCGCCGCTGTTGCCAGGGACAGACTGACTACACTTGACCTTCAAGAGCACTTAGAAGTGGATGGCCTCCAGA 4179
CTCTGTCAGCCTCTGCAGGGGCCACACAAGTCTCCCGAGCCCAAGTCCACAAGCCTCCATGGTTCCCTGGCTCCTCCTCCT 4258
GTGGAGTGCTCCTGTTGATGTCTGAGGTCTGCTTTGGGTACCGCCTGGGAACCTGCTAACCTCCGATGGTCCCTTTGT 4337
GTCCTGTTTACTGTCCTTCTACCTCCAGGTCACCTTAGCTCTGGCTGGGAGTGGGGGTGGGATGCT 4416
GGCTGACCCCCACCTGGTCTGCCAACACAGAACCTGGGGGCTCACACGGGCTCCTGTCTTGCCAAAGCTGGAGCTGAGC 4495
ACACTGGCCCAGGCTGAGTGGGCAGAGCAAAACAAGTGGAAGGGATCTCTCTCCTTAGAGGGAGGTGGCCGAAGGTGT 4574
AGATCCAGCGAGGAGCTGCCATCCCCGCCACCTTCATAGCAGCAAGACCTTCCCATTTCCAATCTCACCTCCAGCAG 4653
GGATATGACTTTGGACAACAAGGCTTTATTTGTAAATATGCTCTTAATATGCAACTTTGAGAAATAAGATAAGAAACATCA 4732
TGTATTTTAAATATAAATGAAGTGTGACACACTGTATACAATTTAATATATATTTTAGGATTTTGTATTATAAGAA 4811
AATGGAATGTGATGTTAACTTTTACAAAAGAGAGAAAATGTTATTTTACTGTTTGAAGAAAATAAATATTCTCA 4890
TTGTTGTAGAAAAAATAAAAAAAGGGCGCGC 4928

Fig. 11

Hum.	MAPPAARLALLSAAALTLAARPA	20	30	40	50	60	70
	SPGLPGPECFTANGADYRGTQNW						
	TALQGGKPCLFWNETFQHPYNT						
Mur.	MAPPAARLALLSAAALTLAARPA	20	30	40	50	60	
	PGPR--SGPECFTANGADYRGTQ						
	SWTALQGGKPCLFWNETFQHPYNT						
Hum.	LKYPNGEGGLGEHNYCRNPDGDV	90	100	110	120	130	140
	SPWCYVAEHEDGVYWKYCEIPACQ						
	MPGNLGCYKDHGNPPPLTGTSKT						
Mur.	LKYPNGEGGLGEHNYCRNPDGDV	90	100	110	120	130	
	SPWCYVAEHEDGVYWKYCEIPACQ						
	MPGNLGCYKDHGNPPPLTGTSKT						
Hum.	SNKLTIQTCISFCRSQRKFAGMES	160	170	180	190	200	210
	GYACFCGNNPDYWKYGEAASTECN						
	SVCFGDHTQPCGGDGRIILFD						
Mur.	SNKLTIQTCISFCRSQRKFAGMES	160	170	180	190	200	
	GYACFCGNNPDYWKHGEAASTECN						
	SVCFGDHTQPCGGDGRIILFD						
Hum.	TLVGACGGNYSAMSSVVYSPDFPD	230	240	250	260	270	280
	TYATGRVCYWTIRVPGASHIHFSF						
	PLFDIRDSADMVELLDGYTHRV						
Mur.	TLVGACGGNYSAMAAVVYSPDFPD	230	240	250	260	270	
	TYATGRVCYWTIRVPGASRIHFNFT						
	LFDIRDSADMVELLDGYTHRV						

Fig.1J

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Hum.  LARFHGRSRPPLSFNVSLDFVILYFFSDRINQAQGFVLYQAVKEELPQERPAVNQTVAEVITEQANLSV
      :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
Mur.  LVRLSGRSRPPPLSFNVSLDFVILYFFSDRINQAQGFVLYQATKEEPPQERPAVNQTLAEVITEQANLSV
      280   290   300   310   320   330   340   350

Hum.  SAARSSKVLYVITTSPPSHPPQTVPGNSWAPPMGAGSHRVEGWTVYGLATLLILTVTAIVAKILLHVTFK
      :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
Mur.  SAAHSSKVLYVITPSPPSHPPQTAQVAIPGHRQLGPTA---TEWKD-GLCTAWRPSSSSQSQQLSQRFFCM
      350   360   370   380   390   400   410

Hum.  SHRVPASGDLRDCHQPGTSGEISIFYKPSSTISIFKKKLKGSQ-QDDRNPLVSD
      430   440   450   460   470

Mur.  SHLNLIESHQETLGTVVVSLGLLEISGPFMSNLPLOSPSLRRSSRVNVNKMTAIPS
      420   430   440   450   460   470

```

Fig.1K

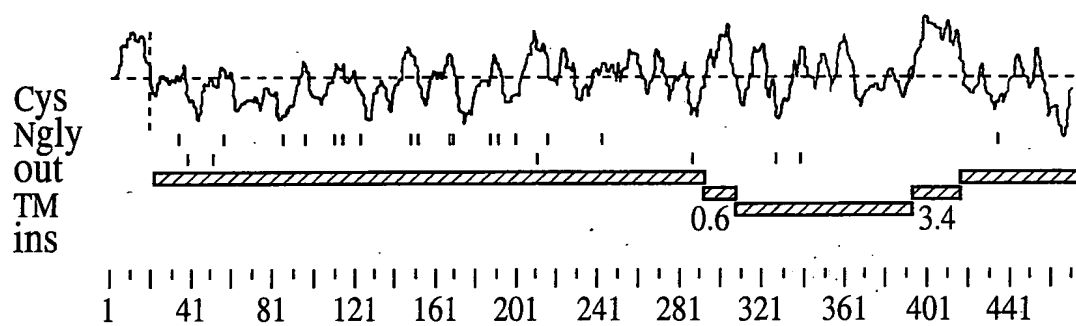


Fig. 1L

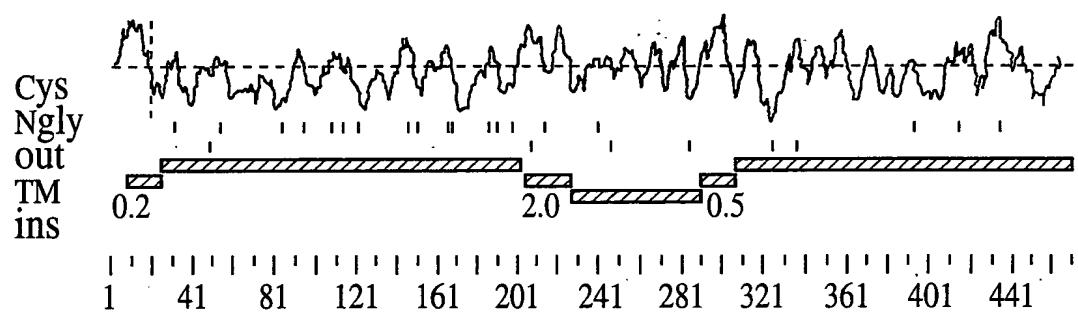


Fig. 1M

	M	M	L	P	Q	N	S	W	H	I	D	F	G	13				
GCGGCCGCTCGCGATCTAGAACTAGTA	ATG	ATG	CTG	CCT	CAA	AAC	TCG	TGG	CAT	ATT	GAT	TTT	GGA	66				
R	C	C	C	H	Q	N	L	F	S	A	V	T	C	I	L	L	N	33
AGA	TGC	TGC	TGT	CAT	CAG	AAC	CTT	TTC	TCT	GCT	GTG	GTA	ACT	TGC	ATC	CTG	CTC	126
S	C	F	L	I	S	S	F	N	G	T	D	L	E	L	R	L	V	53
TCC	TGC	TTT	CTC	ATC	AGC	AGT	TTT	AAT	GGA	ACA	GAT	TTG	GAG	TTG	AGG	CTG	GTC	186
D	G	P	C	S	G	T	V	E	V	K	F	Q	G	Q	W	G	T	73
GAC	GGT	CCC	TGC	TCT	GGG	ACA	GTG	GAG	GTG	AAA	TTC	CAG	GGA	CAG	TGG	GGG	ACT	246
D	D	G	W	N	T	T	A	S	T	V	V	C	K	Q	L	G	C	93
GAT	GAT	GGG	TGG	AAC	ACT	ACT	GCC	TCA	ACT	GTC	GTG	TGC	AAA	CAG	CTT	GGA	TGT	306
S	F	A	M	F	R	F	G	Q	A	V	T	R	H	G	K	I	W	113
TCT	TTC	GCC	ATG	TTT	CGT	TTT	GGA	CAA	GCC	GTG	ACT	AGA	CAT	GGA	AAA	ATT	TGG	366
D	V	S	C	Y	G	N	E	S	A	L	W	E	C	Q	H	R	E	133
GAT	GTT	TCC	TGT	TAT	GGA	AAT	GAG	TCA	GCT	CTC	TGG	GAA	TGT	CAA	CAC	CGG	GAA	426
S	H	N	C	Y	H	G	E	D	V	G	V	N	C	Y	G	E	A	153
AGC	CAT	AAC	TGT	TAT	CAT	GGA	GAA	GAT	GTT	GGT	GTG	AAC	TGT	TAT	GGT	GAA	GCC	486

12/95

Fig. 2A

13 / 95

G	L	R	L	V	D	G	N	N	S	C	S	G	R	V	E	V	K	F	Q	173
GGT	TTG	AGG	CTA	GTG	GAT	GGA	AAC	AAC	TCC	TGT	TCA	GGG	AGA	GTG	GAG	GTG	AAA	TTC	CAA	546
E	R	W	G	T	I	C	D	D	G	W	N	L	N	T	A	A	V	V	C	193
GAA	AGG	TGG	GGG	ACT	ATA	TGT	GAT	GAT	GGG	TGG	AAC	TTG	AAT	ACT	GCT	GCC	GTG	GTG	TGC	606
R	Q	L	G	C	P	S	S	F	I	S	S	G	V	V	N	S	P	A	V	213
AGG	CAA	CTA	GGA	TGT	CCA	TCT	TCT	TTT	ATT	TCT	TCT	GGA	GTT	GTT	AAT	AGC	CCT	GCT	GTA	666
L	R	P	I	W	L	D	D	I	L	C	Q	G	N	E	L	A	L	W	N	233
TTG	CGC	CCC	ATT	TGG	CTG	GAT	GAC	ATT	TTA	TGC	CAG	GGG	AAT	GAG	TTG	GCA	CTC	TGG	AAT	726
C	R	H	R	G	W	G	N	H	D	C	S	H	N	E	D	V	T	L	T	253
TGC	AGA	CAT	CGT	GGA	TGG	GGA	AAT	CAT	GAC	TGC	AGT	CAC	AAT	GAG	GAT	GTC	ACA	TTA	ACT	786
C	Y	D	S	S	D	L	E	L	R	L	V	G	G	T	N	R	C	M	G	273
TGT	TAT	GAT	AGT	AGT	GAT	CTT	GAA	CTA	AGG	CTT	GTA	GGT	GGA	ACT	AAC	CGC	TGT	ATG	GGG	846
R	V	E	L	K	I	Q	G	R	W	G	T	V	C	H	H	K	W	N	N	293
AGA	GTA	GAG	CTG	AAA	ATC	CAA	GGA	AGG	TGG	GGG	ACC	GTA	TGC	CAC	CAT	AAG	TGG	AAC	AAT	906
A	A	A	D	V	V	C	K	Q	L	G	C	G	T	A	L	H	F	A	G	313
GCT	GCA	GCT	GAT	GTC	GTA	TGC	AAG	CAG	TTG	GGA	TGT	GGA	ACC	GCA	CTT	CAC	TTC	GCT	GGC	966
L	P	H	L	Q	S	G	S	D	V	V	W	L	D	G	V	S	C	S	G	333
TTG	CCT	CAT	TTG	CAG	TCA	GGG	TCT	GAT	GTT	GTA	TGG	CTT	GAT	GGT	GTC	TCC	TGC	TCC	GGT	1026

Fig. 2B

N	E	S	F	L	W	D	C	R	H	S	G	T	V	N	F	D	C	L	H	353
AAT	GAA	TCT	TTT	CTT	TGG	GAC	TGC	AGA	CAT	TCC	GGA	ACC	GTC	AAT	TTT	GAC	TGT	CTT	CAT	1086
Q	N	D	V	S	V	I	C	S	D	G	A	D	L	E	L	R	L	A	D	373
CAA	AAC	GAT	GTG	TCT	GTG	ATC	TGC	TCA	GAT	GGA	GCA	GAT	TTG	GAA	CTG	CGA	CTA	GCA	GAT	1146
G	S	N	N	C	S	G	R	V	E	V	R	I	H	E	Q	W	W	T	I	393
GGA	AGT	AAC	AAT	TGT	TCA	GGG	AGA	GTA	GAG	GTG	AGA	ATT	CAT	GAA	CAG	TGG	TGG	ACA	ATA	1206
C	D	Q	N	W	K	N	E	Q	A	L	V	V	C	K	Q	L	G	C	P	413
TGT	GAC	CAG	AAC	TGG	AAG	AAT	GAA	CAA	GCC	CTT	GTG	GTT	TGT	AAG	CAG	CTA	GGA	TGT	CCG	1266
F	S	V	F	G	S	R	R	A	K	P	S	N	E	A	R	D	I	W	I	433
TTC	AGC	GTC	TTT	GGC	AGT	CGT	CGT	GCT	AAA	CCT	AGT	AAT	GAA	GCT	AGA	GAC	ATT	TGG	ATA	1326
N	S	I	S	C	T	G	N	E	S	A	L	W	D	C	T	Y	D	G	K	453
AAC	AGC	ATA	TCT	TGC	ACT	GGG	AAT	GAG	TCA	GCT	CTC	TGG	GAC	TGC	ACA	TAT	GAT	GGA	AAA	1386
A	K	R	T	C	F	R	R	S	D	A	G	V	I	C	S	D	K	A	D	473
GCA	AAG	CGA	ACA	TGC	TTC	CGA	AGA	TCA	GAT	GCT	GGA	GTA	ATT	TGT	TCT	GAT	AAG	GCA	GAT	1446
L	D	L	R	L	V	G	A	H	S	P	C	Y	G	R	L	E	V	K	Y	493
CTG	GAC	CTA	AGG	CTT	GTC	GGG	GCT	CAT	AGC	CCC	TGT	TAT	GGG	AGA	TTG	GAG	GTG	AAA	TAC	1506
Q	G	E	W	G	T	V	C	H	D	R	W	S	T	R	N	A	A	V	V	513
CAA	GGA	GAG	TGG	GGG	ACT	GTG	TGT	CAT	GAC	AGA	TGG	AGC	ACA	AGG	AAT	GCA	GCT	GTT	GTG	1566

14 / 95

Fig. 2C

C K Q L G C G K P M H V F G M T Y F K E 533
 TGT AAA CAA TTG GGA TGT GGA AAG CCT ATG CAT GTG TTT GGT ATG ACC TAT TTT AAA GAA 1626

 A S G P I W L D D V S C I G N E S N I W 553
 GCA TCA GGA CCT ATT TGG CTG GAT GAC GTT TCT TGC ATT GGA AAT GAG TCA AAT ATC TGG 1686

 D C E H S G W G K H N C V H R E D V I V 573
 GAC TGT GAA CAC AGT GGA TGG GGA AAG CAT AAT TGT GTA CAC AGA GAG GAT GTG ATT GTA 1746

 T C S G D A T W G L R L V G G S N R C S 593
 ACC TGC TCA GGT GAT GCA ACA TGG GGC CTG AGG CTG GTG GGC GGC AGC AAC CGC TGC TCG 1806

 G R L E V Y F Q G R W G T V C D D G W N 613
 GGA AGA CTG GAG GTG TAC TTT CAA GGA CGG TGG GGC ACA GTG TGT GAT GAC GGC TGG AAC 1866

 S K A A V C S Q L D C P S S I I G M 633
 AGT AAA GCT GCA GCT GTG GTG TGT AGC CAG CTG GAC TGC CCA TCT TCT ATC ATT GGC ATG 1926

 G L G N A S T G Y G K I W L D D V S C D 653
 GGT CTG GGA AAC GCT TCT ACA GGA TAT GGA AAA ATT TGG CTC GAT GAT GTT TCC TGT GAT 1986

 G D E S D L W S C R N S G W G N N D C S 673
 GGA GAT GAG TCA GAT CTC TGG TCA TGC AGG AAC AGT GGG TGG GGA AAT AAT GAC TGC AGT 2046

 H S E D V G V I C S D A S D M E L R L V 693
 CAC AGT GAA GAT GTT GGA GTG ATC TGT TCT GAT GCA TCG GAT ATG GAG CTG AGG CTT GTG 2106

15/95

Fig. 2D

G G S S R C A G K V E V N V Q G A V G I 713
 GGT GGA AGC AGC AGG TGT GCT GGA AAA GTT GAG GTG AAT GTC CAG GGT GCC GTG GGA ATT 2166

 L C A N G G W G M N I A E V V C R Q L E C 733
 CTG TGT GCT AAT GGC TGG GGA ATG AAC ATT GCT GAA GTT GTT TGC AGG CAA CTT GAA TGT 2226

 G S A I R V S R E P H F T E R T L H I L 753
 GGG TCT GCA ATC AGG GTC TCC AGA GAG CCT CAT TTC ACA GAA AGA ACA TTA CAC ATC TTA 2286

 M S N S G C T G G E A S L W D C I R W E 773
 ATG TCG AAT TCT GGC TGC ACT GGA GGG GAA GCC TCT CTC TGG GAT TGT ATA CGA TGG GAG 2346

 W K Q T A C H L N M E A S L I C S A H R 793
 TGG AAA CAG ACT GCG TGT CAT TTA AAT ATG GAA GCA AGT TTG ATC TGC TCA GCC CAC AGG 2406

 Q P R L V G A D M P C S G R V E V K H A 813
 CAG CCC AGG CTG GTT GGA GCT GAT ATG CCC TGC TCT TCT GGA CGT GTT GAA GTG AAA CAT GCA 2466

 D T W R S V C D S D F S L H A A N V L C 833
 GAC ACA TGG CGC TCT GTC TGT GAT TCT TCT TTC TCT TCT CAT GCT GCC AAT GTG CTG TGC 2526

 R E L N C G D A I S L S V G D H F G K G 853
 AGA GAA TTA AAT TGT GGA GAT GCC ATA TCT CTT TCT TCT GTG GGA GAT CAC TTT GGA AAA GGG 2586

 N G L T W A E K F Q C E G S E T H L A L 873
 AAT GGT CTA ACT TGG GCC GAA AAG TTC CAG TGT GAA GGG AGT GAA ACT CAC CTT GCA TTA 2646

16/95

Fig. 2E

C P I V Q H P E D T C I H S R E V G V 893
 TGC CCC ATT GTT CAA CAT CCG GAA GAC ACT TGT ATC CAC AGC AGA GAA GTT GGA GTT GTC 2706

 C S R Y T D V R L V N G K S Q C D G Q V 913
 TGT TCC CGA TAT ACA GAT GTC CGA CTT GTG AAT GGC AAA TCC CAG TGT GAC GGC CAA GTG 2766

 E I N V L G H W G S L C D T H W D P E D 933
 GAG ATC AAC GTG CTT GGA CAC TGG GGC TCA CTG TGT GAC ACC CAC TGG GAC CCA GAA GAT 2826

 A R V L C R Q L S C G T A L S T T G G K 953
 GCC CGT GTT CTA TGC AGA CAG CTC AGC TGT GGG ACT GCT CTC TCA ACC ACA GGA GGA AAA 2886

 Y I G E R S V R V W G H R F H C L G N E 973
 TAT ATT GGA GAA AGA AGT GTT CGT GTG TGG GGA CAC AGG TTT CAT TGC TTA GGC AAT GAG 2946

 S L L D N C Q M T V L G A P P C I H G N 993
 TCA CTT CTG GAT AAC TGT CAA ATG ACA GTT CTT GGA GCA CCT CCC TGT ATC CAT GGA AAT 3006

 T V S V I C T G S L T Q P L F P C L A N 1013
 ACT GTC TCT GTG ATC TGC ACA GGA AGC CTG ACC CAG CCA CTG TTT CCA TGC CTC GCA AAT 3066

 V S D P Y L S A V P E G S A L I C L E D 1033
 GTA TCT GAC CCA TAT TTG TCT GCA GTT CCA GAG GGC AGT GCT TTG ATC TGC TTA GAG GAC 3126

 K R L R L V D G D S R C A G R V E I Y H 1053
 AAA CGG CTC CGC CTA GTG GAT GGG GAC AGC CGC TGT GCC GGG AGA GTA GAG ATC TAT CAC 3186

17/95

Fig. 2F

D	G	F	W	G	T	I	C	D	D	G	W	D	L	S	D	A	H	V	V	1073
GAC	GGC	TTC	TGG	GGC	ACC	ATC	TGT	GAT	GAC	GGC	TGG	GAC	CTG	AGC	GAT	GCC	CAC	GTG	GTG	3246
C	Q	K	L	G	C	G	V	A	F	N	A	T	V	S	A	H	F	G	E	1093
TGT	CAA	AAG	CTG	GGC	TGT	GGA	GTG	GCC	TTC	AAT	GCC	ACG	GTC	TCT	GCT	CAC	TTT	GGG	GAG	3306
G	S	G	P	I	W	L	D	D	L	N	C	T	G	T	E	S	H	L	W	1113
GGG	TCA	GGG	CCC	ATC	TGG	CTG	GAT	GAC	CTG	AAC	TGC	ACA	GGA	ACG	GAG	TCC	CAC	TTG	TGG	3366
Q	C	P	S	R	G	W	G	Q	H	D	C	R	H	K	E	D	A	G	V	1133
CAG	TGC	CCT	TCC	CGC	GGC	TGG	GGG	CAG	CAC	GAC	TGC	AGG	CAC	AAG	GAG	GAC	GCA	GGG	GTC	3426
I	C	S	E	F	T	A	L	R	L	Y	S	E	T	E	T	E	S	C	A	1153
ATC	TGC	TCA	GAA	TTC	ACA	GCC	TTG	AGG	CTC	TAC	AGT	GAA	ACT	GAA	ACA	GAG	AGC	TGT	GCT	3486
G	R	L	E	V	F	Y	N	G	T	W	G	S	V	G	R	R	N	I	T	1173
GGG	AGA	TTG	GAA	GTC	TTC	TAT	AAC	GGG	ACC	TGG	GGC	AGC	GTC	GGC	AGG	AGG	AAC	ATC	ACC	3546
T	A	I	A	G	I	V	C	R	Q	L	G	C	G	E	N	G	V	V	S	1193
ACA	GCC	ATA	GCA	GGC	ATT	GTG	TGC	AGG	CAG	CTG	GGC	TGT	GGG	GAG	AAT	GGA	GTT	GTC	AGC	3606
L	A	P	L	S	K	T	G	S	G	F	M	W	V	D	D	I	Q	C	P	1213
CTC	GCC	CCT	TTA	TCT	AAG	ACA	GGC	TCT	GGT	TTC	ATG	TGG	GTG	GAT	GAC	ATT	CAG	TGT	CCT	3666
K	T	H	I	S	I	W	Q	C	L	S	A	P	W	E	R	R	I	S	S	1233
AAA	ACG	CAT	ATC	TCC	ATA	TGG	CAG	TGC	CTG	TCT	GCC	CCA	TGG	GAG	CGA	AGA	ATC	TCC	AGC	3726

18 / 95

Fig. 2G

P	A	E	E	T	W	I	I	T	C	E	D	R	I	R	V	R	G	G	D	T	1253
CCA	GCA	GAA	GAG	ACC	TGG	ATC	ACA	TGT	GAA	GAT	AGA	ATA	AGA	GTG	CGT	GGA	GGA	GAC	ACC	3786	
E	C	S	G	R	V	E	I	W	H	A	G	S	W	G	T	V	C	D	D	1273	
GAG	TGC	TCT	GGG	AGA	GTG	GAG	ATC	TGG	CAC	GCA	GGC	TCC	TGG	GGC	ACA	GTG	TGT	GAT	GAC	3846	
S	W	D	L	A	E	A	E	V	V	C	Q	Q	L	G	C	G	S	A	L	1293	
TCC	TGG	GAC	CTG	GCC	GAG	GCG	GAA	GTG	GTG	TGT	CAG	CAG	CTG	GGC	TGT	GGC	TCT	GCT	CTG	3906	
A	A	L	R	D	A	S	F	G	Q	G	T	G	T	I	W	L	D	D	M	1313	
GCT	GCC	CTG	AGG	GAC	GCT	TCG	TTT	GGC	CAG	GGA	ACT	GGA	ACC	ATC	TGG	TTG	GAT	GAC	ATG	3966	
R	C	K	G	N	E	S	F	L	W	D	C	H	A	K	P	W	G	Q	S	1333	
CGG	TGC	AAA	GGA	AAT	GAG	TCA	TTT	CTA	TGG	GAC	TGT	CAC	GCC	AAA	CCC	TGG	GGA	CAG	AGT	4026	
D	C	G	H	K	E	D	A	G	V	R	C	S	G	Q	S	L	K	S	L	1353	
GAC	TGT	GGA	CAC	AAG	GAA	GAT	GCT	GGC	GTG	AGG	TGC	TCT	GGA	CAG	TCG	CTG	AAA	TCA	CTG	4086	
N	A	S	S	G	H	L	A	L	I	L	S	S	I	F	G	L	L	L	L	1373	
AAT	GCC	TCC	TCA	GGT	CAT	TTA	GCA	CTT	ATT	TTA	TCC	AGT	ATC	TTT	GGG	CTC	CTT	CTC	CTG	4146	
V	L	F	I	L	F	L	T	W	C	R	V	Q	K	Q	K	H	L	P	L	1393	
GTT	CTG	TTT	ATT	CTA	TTT	CTC	ACG	TGG	TGC	CGA	GTT	CAG	AAA	CAA	AAA	CAT	CTG	CCC	CTC	4206	
R	V	S	T	R	R	R	G	S	L	E	E	N	L	F	H	E	M	E	T	1413	
AGA	GTT	TCA	ACC	AGA	AGG	AGG	GGT	TCT	CTC	GAG	GAG	AAT	TTA	TTC	CAT	GAG	ATG	GAG	ACC	4266	

19/95

Fig. 2H

C L K R E D P H G T R T S D D T P N H G 1433
TGC CTC AAG AGA GAG GAC CCA CAT GGG ACA AGA ACC TCA GAT GAC ACC CCC AAC CAT GGT 4326

C E D A S D T S L L L G V L P A S E A T K 1453
TGT GAA GAT GCT AGC GAC ACA TCG CTG TTG GGA GTT CTT CCT GCC TCT GAA GCC ACA AAA 4386

* 1454
TGA 4389

CTTTAGACTTCCAGGGCTCACCAGATCAACCTCTAAATATCTTTGAAGGAGACAACTTTTAAATGAATAAAGAGGA 4468
AGTCAAGTTGCCCTATGGAAAACCTTGCCAAATAACATTTCTTGAACAATAGGAGAACACAGCTAAATTGATAAAGACTGG 4547
TGATAATAAAAAATTGAATTATGTATATCACTGTTAAAAAAAACGACGCGTGGTTCG 4626
AC 4628

Fig. 2I

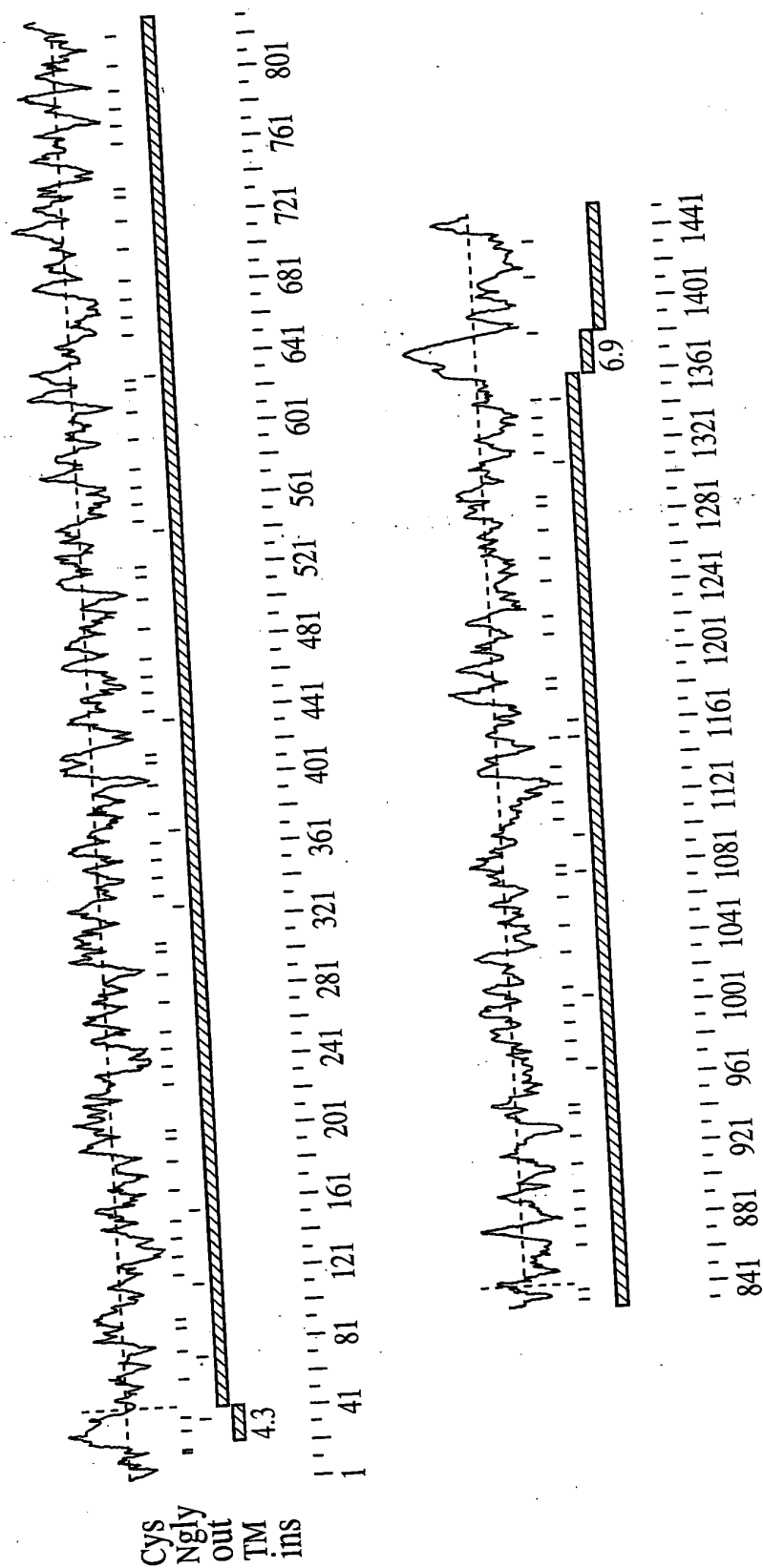


Fig. 2J

Hum.	MMLPQNSWHIDFGRCCCHQNLFS	AVT	CILLNSCFLISSFN	GTDL	ELRLVNGD	GPCSGT	VEVKFQ	QGWG	
WC1	MAL-----GR---	HLSLRGL---	CVLL	LLGT--	MVG---	GQALELRLK	DGVHRC	EGRVEVKHQGEWG	
	10	20	30	40	50	60	70		
Hum.	TVCDDGWN	TTASTV	VCKQLG	CPFS	FAMR	FGQAV	TR-HGKI	WLDDVSCYGNESALWECQH---	REWGSHN
WC1	TVDGYR	WTLK	DASV	VC	RLG	CGAAIG-F	PGAY	FGPGLGPIWLLY	TSCEGT
	80	90	100	110	120	130			
Hum.	CYHG	EDV	GVNCY	GEAN	LGLRL	VDGNN	SCSR	VEVKFQ	ERWGTICDDGWN
WC1	YNHGR	DAGV	VCSG---	FVRL	AGD	GPCSGR	VEVH	SGEAWIPVSD	GNFTLATAQII
	140	150	160	170	180	190	200		
Hum.	VVNS	PAVLR	PIW	DDIL	CQGN	ELALWNC	HRGW	GNHDCSHN	EDVTIL
WC1	HEL	FRESSA	QVWAE	EFR	CEGE	EPELW	VCPR	PCPGTCHH	SGSAQVCSAY
	210	220	230	240	250	260	270		
	190	200	210	220	230	240	250		

Fig. 2K

```

280      290      300      310      320      330      340
Hum.  LKIQRWGTVCHHKWNNAAADVCKQLGCGTALHFAGLPHLQSGDVVWLDGVSCSGNESFLWDCRHS
      .. : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  MNISQWRALCASHWSLANANVICRQLGCGVAISTPGPHLVEEGDQILTARFHCSGAESFLWSCPV
260      270      280      290      300      310      320

350      360      370      380      390      400      410
Hum.  VNFDCLHQNDVSVICSDGADLELRADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFS
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GGPDCSHGNTASVICS-GNQI-----QVLPQCND-----SV
330      340      350

420      430      440      450      460      470      480
Hum.  FGSRRAKPSNEARDIWINISISCTGNESALWDCTYDGKAKRTCRRSDAGVICSDKADLRLVGAHSPCY
      ..... : : : : : : : : : : : : : : : : : : : : : :
WC1  -----SPTGSA-----ASEDSA---PY-----CSDSRQL--RLVDGGGPCA
360      370      380

490      500      510      520      530      540      550
Hum.  GRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GRVEILDQGSWGTICDDGWDLDDARVVCRQLGCCGEALNATGSAHFGAGSGPIWLDNLNCTGKESHVWRCP
390      400      410      420      430      440      450

```

Fig. 2L

Fig. 2M

840	850	860	870	880	890	900
Hum.	NCGDAISLSVGDHFGKGNGLTWA	KFQCEGSETHALCPIVQHPEDTC	HSREVG	VVCSRYTDVRLV-NG		
	:: ::::	: ::::	: ::::	: ::::	: ::::	: ::::
WC1	GCGKAVSVLGHMPFRES	DGQVAAEFRC	DGGEPELWSCPRVPCPGGT	CLHSGAAQVVC	SVYTEVQLMKNG	
	740	750	760	770	780	790
						800
910	920	930	940	950	960	970
Hum.	KSQCDGQVEINVLGHWGSLCDTHWD	PEDARVLCRQLSCGTALSTTG	GKYIGERSVRVW	GHRFHC	CLGNESL	
	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::
WC1	TSQCEGQVEMKISGRWRALCASHW	SLANANVVCRLGCGVAISTPR	GPHLVEG	GDQISTAQFHCSGAESF		
	810	820	830	840	850	860
						870
980	990	1000	1010	1020	1030	1040
Hum.	LDNCQMTVLGAPPCIHGNTVSVICTG	SLTQPLFPCLANVSDPYLSAV	PEGSALICLEDKRLRLVDGDSRC			
	: ::::	: ::::	: ::::	: ::::	: ::::	: ::::
WC1	LWSCPVTALGGPDCSHGNTASVICS	GNHTQVLPQCNDFLSQPAGSAA	SESSPYCSDSRQLRLVDGGGPC			
	880	890	900	910	920	930
						940
1050	1060	1070	1080	1090	1100	1110
Hum.	AGRVEIYHDFWGTICDDGWDLS	DAHVVQC	KLGC	GVAFNATVSAHFGE	SGPIWLDDDLNCTGTESHLWQC	
	: ::::	: ::::	: ::::	: ::::	: ::::	: ::::
WC1	GGRVEILDQGSWGTICDDDWDL	DDARVVCRLGCC	GEALNATGSAHF	GAGSGPIWLDDDLNCTGKESHVWRC		
	950	960	970	980	990	1000
						1010

Fig. 2N

Fig. 20

```

1370      1380      1390      1400      1410
Hum.  LSSIFGLLLVLFILFTWCRVQK-----QKHLPLRVS-----TRRRG-----SLEENLFHEME
      :... :...: . . : :... . . : :... : . . . . . :
WC1  IGSLFLVLVILVTQLLRW-RAERRALSSYEDALAEAVYEELDYLLTQKEGLGSPDQMTDVPDENYDDAE
1290      1300      1310      1320      1330      1340      1350

      1420      1430      1440
Hum.  TC-----LKDREDPHGTRTSD-----DTPNHGCEDAS-----DTSLLGV
      . : . . : . : . . : . . : . . : . . : . . : . . : . . :
WC1  EVPVPGTSPSPSQNEEEVPPPEKEDGVRSSQTGSFLNFSREAAANPGEGEESFWLLQGGKGDAGYDDVELSA
1360      1370      1380      1390      1400      1410      1420

1450
Hum.  LPASEAT-K
      : . : . :
WC1  LGTSPVTFS
1430

```

Fig. 2P

1

1. **Introduction**
 2. **Methodology**
 3. **Results**
 4. **Discussion**
 5. **Conclusion**
 6. **References**
 7. **Appendix**
 8. **Index**
 9. **Glossary**
 10. **Notes**
 11. **Footnotes**
 12. **Endnotes**
 13. **Supplementary Material**
 14. **Tables**
 15. **Figures**
 16. **Equations**
 17. **Formulas**
 18. **Diagrams**
 19. **Charts**
 20. **Graphs**
 21. **Tables**
 22. **Figures**
 23. **Equations**
 24. **Formulas**
 25. **Diagrams**
 26. **Charts**
 27. **Graphs**
 28. **Tables**
 29. **Figures**
 30. **Equations**
 31. **Formulas**
 32. **Diagrams**
 33. **Charts**
 34. **Graphs**
 35. **Tables**
 36. **Figures**
 37. **Equations**
 38. **Formulas**
 39. **Diagrams**
 40. **Charts**
 41. **Graphs**
 42. **Tables**
 43. **Figures**
 44. **Equations**
 45. **Formulas**
 46. **Diagrams**
 47. **Charts**
 48. **Graphs**
 49. **Tables**
 50. **Figures**
 51. **Equations**
 52. **Formulas**
 53. **Diagrams**
 54. **Charts**
 55. **Graphs**
 56. **Tables**
 57. **Figures**
 58. **Equations**
 59. **Formulas**
 60. **Diagrams**
 61. **Charts**
 62. **Graphs**
 63. **Tables**
 64. **Figures**
 65. **Equations**
 66. **Formulas**
 67. **Diagrams**
 68. **Charts**
 69. **Graphs**
 70. **Tables**
 71. **Figures**
 72. **Equations**
 73. **Formulas**
 74. **Diagrams**
 75. **Charts**
 76. **Graphs**
 77. **Tables**
 78. **Figures**
 79. **Equations**
 80. **Formulas**
 81. **Diagrams**
 82. **Charts**
 83. **Graphs**
 84. **Tables**
 85. **Figures**
 86. **Equations**
 87. **Formulas**
 88. **Diagrams**
 89. **Charts**
 90. **Graphs**
 91. **Tables**
 92. **Figures**
 93. **Equations**
 94. **Formulas**
 95. **Diagrams**
 96. **Charts**
 97. **Graphs**
 98. **Tables**
 99. **Figures**
 100. **Equations**
 101. **Formulas**
 102. **Diagrams**
 103. **Charts**
 104. **Graphs**
 105. **Tables**
 106. **Figures**
 107. **Equations**
 108. **Formulas**
 109. **Diagrams**
 110. **Charts**
 111. **Graphs**
 112. **Tables**
 113. **Figures**
 114. **Equations**
 115. **Formulas**
 116. **Diagrams**
 117. **Charts**
 118. **Graphs**
 119. **Tables**
 120. **Figures**
 121. **Equations**
 122. **Formulas**
 123. **Diagrams**
 124. **Charts**
 125. **Graphs**
 126. **Tables**
 127. **Figures**
 128. **Equations**
 129. **Formulas**
 130. **Diagrams**
 131. **Charts**
 132. **Graphs**
 133. **Tables**
 134. **Figures**
 135. **Equations**
 136. **Formulas**
 137. **Diagrams**
 138. **Charts**
 139. **Graphs**
 140. **Tables**
 141. **Figures**
 142. **Equations**
 143. **Formulas**
 144. **Diagrams**
 145. **Charts**
 146. **Graphs**
 147. **Tables**
 148. **Figures**
 149. **Equations**
 150. **Formulas**
 151. **Diagrams**
 152. **Charts**
 153. **Graphs**
 154. **Tables**
 155. **Figures**
 156. **Equations**
 157. **Formulas**
 158. **Diagrams**
 159. **Charts**
 160. **Graphs**
 161. **Tables**
 162. **Figures**
 163. **Equations**
 164. **Formulas**
 165. **Diagrams**
 166. **Charts**
 167. **Graphs**
 168. **Tables**
 169. **Figures**
 170. **Equations**
 171. **Formulas**
 172. **Diagrams**
 173. **Charts**
 174. **Graphs**
 175. **Tables**
 176. **Figures**
 177. **Equations**
 178. **Formulas**
 179. **Diagrams**
 180. **Charts**
 181. **Graphs**
 182. **Tables**
 183. **Figures**
 184. **Equations**
 185. **Formulas**
 186. **Diagrams**
 187. **Charts**
 188. **Graphs**
 189. **Tables**
 190. **Figures**
 191. **Equations**
 192. **Formulas**
 193. **Diagrams**
 194. **Charts**
 195. **Graphs**
 196. **Tables**
 197. **Figures**
 198. **Equations**
 199. **Formulas**
 200. **Diagrams**
 201. **Charts**
 202. **Graphs**
 203. **Tables**
 204. **Figures**
 205. **Equations**
 206. **Formulas**
 207. **Diagrams**
 208. **Charts**
 209. **Graphs**
 210. **Tables**
 211. **Figures**
 212. **Equations**
 213. **Formulas**
 214. **Diagrams**
 215. **Charts**
 216. **Graphs**
 217. **Tables**
 218. **Figures**
 219. **Equations**
 220. **Formulas**
 221. **Diagrams**
 222. **Charts**
 223. **Graphs**
 224. **Tables**
 225. **Figures**
 226. **Equations**
 227. **Formulas**
 228. **Diagrams**
 229. **Charts**
 230. **Graphs**
 231. **Tables**
 232. **Figures**
 233. **Equations**
 234. **Formulas**
 235. **Diagrams**
 236. **Charts**
 237. **Graphs**
 238. **Tables**
 239. **Figures**
 240. **Equations**
 241. **Formulas**
 242. **Diagrams**
 243. **Charts**
 244. **Graphs**
 245. **Tables**
 246. **Figures**
 247. **Equations**
 248. **Formulas**
 249. **Diagrams**
 250. **Charts**
 251. **Graphs**
 252.

Fig. 2Qi

```

280      290      300      310      320      330      340
Hum.  TCTTTCGCCATGTTTCGTTTTGGACAAGCCGTGA--CTAGACATGGAAAAATTTGGCTTGATGATGTTTC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   GCCATTG--GTTTCCCTGGAGGGGCTTATTTTGGGCCAGGACTTGGCCCCCATTGGCCTTTTGATATACTTC
220      230      240      250      260      270      280
      350      360      370      380      390      400      410
Hum.  CTGTTATGGAATGAGTCAGCTCTCTGGGAATGTCAACACCGGGAATGGGGAAGCCATAACTGTTATCAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   ATGTGAAGGGACAGAGTCAACTGTCAGTGACTGTGAGCAT-TCTAATATTAAAGAC-TATC-GTAATGAT
290      300      310      320      330      340      350
      420      430      440      450      460      470      480
Hum.  GGAGAAGATGTTGGTGTGAACTGTTATGTTGGAAGCCAA-TCTGGGTTTGAG--GCTAG-TGGATGGAAAC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   GGCTATAATCATGGTCGGGA--TGCTGGAGTAGTCTGCTCAGGATTTGTGCGTCTGGCTGGAGGGGATG
360      370      380      390      400      410      420
      490      500      510      520      530      540      550
Hum.  AACTCCTGTTCAGGGAGAGTGGAGGTGAAATTCCAAGAAAGGTGGGGACTATATGTGATGATGGGTGGA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   GAC-CCTGCTCAGGGCGAGTAGAAGTGCATT--CTGGAGAAGCTTGGATCCCAGTGT-CTGATGGGAACT
430      440      450      460      470      480

```

Fig. 2Qⁱⁱⁱ

```

560      570      580      590      600      610      620
Hum.  ACTGAAATACTGCTGCCGTGGTGTGCAGGCAACTAGGATGTCCATCTTCTTTATTCTTCTGGAGTTGT
      .. . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   TCACACTTGCCACTGCC-----CAG-----ATCATCTGT-----GCAGAGTTGGG
490      500      510      520

630      640      650      660      670      680      690
Hum.  TAATAGCCCTGCTGTATTGCGCCCCCATTTGGCTGGATGACATTTTATGCCAGGGAATGAGTTGGCACT-
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   TTGTGGC-----AAGGCTG--TGTCTGT-----CCTGGGACATGAG-----CTCTT
530      540      550      560

700      710      720      730      740      750      760
Hum.  CTGGAATTGCAGACATCGTGGATGGGAAATCATGACTGCAGTCACAATGAGGATGTCACATTAACTTGT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   CAGAGAGTCCAGT-GCC-----CAGGTCTG--GGC---TGAAGAGTTCA-----GG
570      580      590      600

770      780      790      800      810      820      830
Hum.  TATGATAGTAGTGATCTTGAACCTAAGGCTTGTAGGTGGAACCTAACCGCTGTATGGGGAGAGTAGAGCTGA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   TGTGAGGGGAGGAGCCTGAGCT---CT-----GGGTCTGCCCC-CAGAGTG-----CCCTG-
610      620      630      640      650

```

Fig. 2Qiii

```

      840      850      860      870      880      890      900
Hum.  AAATCCAAGGAGGTGGGGACCGGTATGCCACCATAAGTGGAACAATGCTGCAGCTGATGTCGTATGCAA
      ::::: ::::: ::::: ::::: ::::: ::::: :::::
WC1  ---TCCA-----GGGGCACGTGT--CACCACA-GTGGATC--TGCT-CAGGTTGTTTGTTCAGCAT
      660      670      680      690      700

      910      920      930      940      950      960      970
Hum.  GCAGTTGGGATGTGGAACCGCACTTCACCTTCGCTGGCTTGCCCTCATTTGCAGTCAGGGTCTGATGTTGTA
      ..      .:::. : ::::: : ::::: : ::::: : ::::: : :::::
WC1  ACT-----CAGAAGTCCGGCTCATGACAA-AC-GGCT--CCTC-TCAG-TGTGAAGGGCAGGTGGAGAT
      710      720      730      740      750      760

      980      990      1000      1010      1020      1030      1040
Hum.  TGGCTTGATGGTGTCTCCTGTCTCCGGTAATGAATCTTTTCTTTGGGACTGCAGACATTCCGGAACCGTCA
      :::::   ::   ::   ::::: : ::::: : ::::: : ::::: :
WC1  GAACATT-----TCTG-GACAATGGAGAGCGCTCTGTGCCCTCCC-CTGGAGTCTGGCCCAATGCC---A
      770      780      790      800      810      820

      1050      1060      1070      1080      1090      1100      1110
Hum.  ATTTGACTGTCTTCATCAAAACGATGTGTCTGTGATCTGCTCAGATGGAGCAGATTGGAACCTGCGACT
      :: ::::: ::::: ::::: ::::: ::::: :::::
WC1  ATGTTATCTGTCGTACGCTCGGCTGTGGAGTTGCCATCTCCACCCCGGAG-----GACCAC-ACT
      830      840      850      860      870      880

```

Fig. 2Qiv

```

1120      1130      1140      1150      1160      1170      1180
Hum. AGCAGATGGAAGTAACAATTGTTTCAGGGAGAGTAGAGGTGAGAAATTCA-TGAACAGTGGTGGACAATATG
  :: ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
WC1 TG---GTGGAAGAAG---GTGATCAG--ATCCTAACAGCCCGATTTCACCTGCTCTG-----GGGC-----TG
      890      900      910      920      930

1190      1200      1210      1220      1230      1240      1250
Hum. TGACCAGAACTGGAAGAATGAACAAGCCCTTGTGGTTTGTAAAGCAGCTAGGATGTCCGTTTCAGCGTCTTT
  ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
WC1 AGTCCT-TCCTGTGGAGTTGT-----CCT-GTGACT-----GCC-CTGGGTGGTCTGCTGACTGTTCCCAT
      940      950      960      970      980      990

1260      1270      1280      1290      1300      1310      1320
Hum. GGCAG-TCGTCGTGCTAAACCTAGTAATGAAGCTAGAGACATTGGATAAACAGCATATCTTGCACCTGGG
  ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
WC1 GGCAACACAGCCTCTGTGATCTGTCTCAGGAAACCAGATCCAGGTGCTTCCCCCAGTGCAACGA-CTCCG--
      1000      1010      1020      1030      1040      1050      1060

1330      1340      1350      1360      1370      1380      1390
Hum. AATGAGTCAGCTCTCTGGGACTGCACATATGATGGAAAAGCAAAGCGAACATGCTTCCGAAGATCAGATG
  ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
WC1 --TGCTCAACCTACAGGCTCTGC-----GGC-----CTCAGAGGACA-GCGCCC-----CCTACTG
      1070      1080      1090      1100

```

Fig. 2Q^v


```

1400      1410      1420      1430      1440      1450      1460
Hum. CTGGAGTAATTGTTCTGATAAGGCAGATCTGGACCTAAGGCTTGTCGGGGCTCATAGCCCCCTGTTATGG
    :: ...      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1 CTCAGA-----CAG--CAGGCAGCTCCG--CCTGGTG---GACGGGG-GC--GGTCCCTGCGCCGG
1110      1120      1130      1140      1150      1160

1470      1480      1490      1500      1510      1520
Hum. GAGATTGGAGGTGAAATACCAAGGAGAGTGGGGGACTGTGTGTCATGACAGATGGAGCACAAAGG-AATGC
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1 GAGAGTGGAGATCCTTGACCAAGGCTCCTGGGGCACCATCTGTGATGACGGCTGGGAC-CTGGACGATGC
1170      1180      1190      1200      1210      1220

1530      1540      1550      1560      1570      1580      1590
Hum. A-GCTGTTGTGTGTAACAATTGGGATGTGGA-AAGCCTATGCAATGTGTTGGTATGACCTATTTAAAG
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1 CCGC-GTGGTGTGCAGGCAGCTGGGCTGTGGAGAAGCCCTCA-ATGCCACGGGGTCTGCTCACTTCGGGG
1230      1240      1250      1260      1270      1280      1290

1600      1610      1620      1630      1640      1650      1660
Hum. AAGCATCAGGACCTATTGGCTGGATGACGTTTCTTGCAATGGAAATGAGTCAAAATATCTGGGACTGTGA
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1 CAGGATCAGGGCCCATCTGGTTGGACAACTTGAAGTGCACAGGAAAGGAGTCCCACGTGTGGAGGTGCCC
1300      1310      1320      1330      1340      1350      1360

```

Fig. 2Qvi

```

1670      1680      1690      1700      1710      1720      1730
Hum. ACACAGTGGATGGGAAAGCATAATTGTGTACACAGAGAGGATGTGATTGTAACCTGCTCAGGTGATGCA
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 TTCCCGGGGCTGGGGCAGCACAACTGCAGACACAAAGCAGGACGCGGGGTCACTCTGCTCAG--AGTTC-
1370      1380      1390      1400      1410      1420      1430

1740      1750      1760      1770      1780      1790      1800
Hum. ACATGGGGCCTGAGGCTGGTGGGGCGCAGCAACCGCTGCTCGGGAAGACTGGAGGTGTACTTTCAAGGAC
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 -CT--GGCCCTCAGGATGGTGAGTGAGGACCAGCAGTGTGCTGGTGGTGGAGTTTTCTACAATGGGA
1440      1450      1460      1470      1480      1490      1500

1810      1820      1830      1840      1850      1860      1870
Hum. GGTGGGGCACAGTGTGTGATGACGGCTGGAACAGTAAGCTGCAGCTGTGGTGTAGCCAGCTGGACTG
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 CCTGGGGCAGTGTCTGCGGTAAACCCCATGGAAGACATCACTGTGTCCACGATCTGCAGACAGCTTGGCTG
1510      1520      1530      1540      1550      1560      1570

1880      1890      1900      1910      1920      1930      1940
Hum. CCCATCTTCTATCATTTGGCATGGGTCTG-GGAAACGCTTCTA-CAGGATATGGAATAATTGGCTCGATG
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 T--GGGGACAGTGGAAACCCCTCAACTCTTCTGTGCTCTTAGAGAGAGGTTTAGGCCACAGTGGGTGGAT-
1580      1590      1600      1610      1620      1630

```

Fig. 2Qviii

```

1950      1960      1970      1980      1990      2000      2010
Hum.  ATGTTTCCCTGTGATGGAGATGAGTCAGATCTCTGTGTCATGCAGGAACAGTGGGTG--GGGAAATAATGAC
      ..... : : : : : : : : : : : : : : : : : : : : : : : :
WC1  -AGAAATCCAGTGTCCGAAAACTGACACCTCTCT--CTGGCAGTGTCCCTTCTGACCCCTTGGAAATTACAAC
1640      1650      1660      1670      1680      1690      1700

      2020      2030      2040      2050      2060      2070      2080
Hum.  TGCAGTCACAGTGAAGATGTTGGAGTG-ATCTGTTCTGATG-CATCGGATATGAGCTGAGGCTTGTGGG
      : : : : : : : : : : : : : : : : : : : : : : : :
WC1  T-CATGCTCTCCAAAGGAGGAAGCCCTATATCTGGTGTGCAGACAGCAGACA--GATCCGC--CTGGTGGA
1710      1720      1730      1740      1750      1760

      2090      2100      2110      2120      2130      2140      2150
Hum.  TGAAGCAGCAGGTGTGCTGGAAAAGTTGAGGTGAATGTCCAGGGTGCCGTGGGAATTCGTGTGCTAAT
      : : : : : : : : : : : : : : : : : : : : : : : :
WC1  TGGAGGTGTCGCTGCTCTGGGAGAGTGGAGATCCTTGACCAGGGCTCCTGGGGCACCATCTGTGATGAC
1770      1780      1790      1800      1810      1820      1830

      2160      2170      2180      2190      2200      2210      2220
Hum.  GGCTGGGAATGAACATTGCTGAAGTTGTTGCAGGCAACTTGAATGTGGTCTGCAATCAGGGTCTCCA
      : : : : : : : : : : : : : : : : : : : : : : : :
WC1  CGCTGGGACCTGGACGATGCCCGTGTGGTGTGCAAGCAGCTGGGCTGTGGAGAAGC---CCTGGACGCCCA
1840      1850      1860      1870      1880      1890      1900

```

Fig. 2Qviii

```

2230      2240      2250      2260      2270      2280
Hum.  GAGA-GCCTCATTTACAGAA--AGAACATTACACATCTTAATGTCGAATCTGGCTGCACCTGGAGGGGA
      .:. : : : .:.:. .:.:. . : : : . : : .:. .:.:. .:.:.:. .:.:.:.
WC1  CTGTCTCTTCCCTTTCGGACGGGATCAGGGCCCATCTGGCTGGATGAAGTGAACCTGCAGAGGAGAGGA
1910      1920      1930      1940      1950      1960      1970

2290      2300      2310      2320      2330      2340      2350
Hum.  AGCCTCTCTCTGGGATTGTATACGATGGGAGTGGAAACAG-ACTGCGTGTCAATTAAATATGGAAGCAAG
      . : : : : . : : : : . : : : : . : : : : . : : : : . : : : : . : : : :
WC1  GTCCCAAGTATGAGGTGCCCTTCCTGGGGATGGCGGCAACACAAC-TGCAATCATCAAGAAGATGCAGG
1980      1990      2000      2010      2020      2030      2040

2360      2370      2380      2390      2400      2410      2420
Hum.  TTGATCTGCTCAGCCACAGGCAGCCAGGCTGTTGGAGCTGATATGCCCTGCTCTGGACGTGTGAA
      . : : : : . : : : : . : : : : . : : : : . : : : : . : : : : . : : : :
WC1  AGTCATCTGCTCAGGATTTGTGC-----GTCTGGCTGGAGGAGATGGACCCCTGCTCAGGGCGAGTAGAA
2050      2060      2070      2080      2090      2100

2430      2440      2450      2460      2470      2480      2490
Hum.  GTGAACATGCAGACACATGGCGCTCTGTCTGTGATTCTGATTCTCTCTCTCATGCTGCCAATGT--GCT
      . : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GTGCATTCTGGAGAAAGCCTGGACCCAGTGTCTGTATGGAACCTTCACACTCCCCACTGCCCAGGTCATCT
2110      2120      2130      2140      2150      2160      2170

```

Fig. 2Qix

	2500	2510	2520	2530	2540	2550	2560
Hum.	GTGCAGAGAA	TAAATTGTGGAGATGCCATA	TCTTCTTCTGTGGGAGATCACT	TTGGAAAAGGG	-AATGG		

WC1	GTGCAGAGC	--TGGGATGTGGCAAGGCTGTGTCT	-GTCCTGGGACACATGCCATT	CAAGAGATCCGATGG			
	2180	2190	2200	2210	2220	2230	2240
	2570	2580	2590	2600	2610	2620	2630
Hum.	TCTAACTTGGGCCGAAAAGTTCCAGTGTGAAGGAGTGAAACT	CACCTTGCATTATGCCCCATTGTTCAA					

WC1	CCAGGTC	TGGGCTGAAGAGTTCAGGTGTGATGGGGGGAGCCTGAGCTCTGGTCT	GCCCCAGAGTGCCC				
	2250	2260	2270	2280	2290	2300	2310
	2640	2650	2660	2670	2680	2690	2700
Hum.	CATCCGGAAGACACTTGTATCCACAGCAGAGAGTTGGAGTTGTCTGTCCCGATA	TACAGATGTC	CGAC				

WC1	TGTCCAGGAGGCACATGTCTCCACAGTGGAGCTGCTCAGGTTGTCTGTTCAGTGTACACAGAA	GTC	CAGC				
	2320	2330	2340	2350	2360	2370	2380
	2710	2720	2730	2740	2750	2760	2770
Hum.	TTGTGAATGGCAAATCC	---CAGTGTGACGGGCAAGTGGAGATCAACGTGCT	-TGGACACTGGGGCTCAC				

WC1	TTATGAAAAACGGCACCTCTCAATGTGAGGGCAGGTGGAGAT	-GAAGATCTCTGGACGATGGAGAGCGC					
	2390	2400	2410	2420	2430	2440	2450

Fig. 2Qx

```

2780      2790      2800      2810      2820      2830      2840
Hum.  TGTGTGACACCCACTGGGACCCAGAAAGATGCCCGTGTTCATATGCAGACAGCTCAGCTGTGGGACTGCTCT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  TCTGTGCCCTCCCACTGGAGTCTGGCCAATGCCCAATGTTGTCTGTCTGTCTCAGCTCGGCTGTGGAGTCGCCAT
2460      2470      2480      2490      2500      2510      2520

2850      2860      2870      2880      2890      2900      2910
Hum.  CTCAACCCACAGGAGGAAAATATATTGGAGAAAGAGTGTTCGTGTGTGGGACACAGGTTTCATTGCTTA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  CTCCACCCCCAGAGGACCACTTGGTGAAGGAGGTGATCAGATCTCAACAGCCCCAATTTCACCTGCTCA
2530      2540      2550      2560      2570      2580      2590

2920      2930      2940      2950      2960      2970      2980
Hum.  GGGAATGAGTCACCTCTGGATAAAGTGTCAAAATGACAGTTCTTGGAGCACCTCCCTGTATCCATGGAAATA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GGGGCTGAGTCCTTCCTGTGGAGTTGTCCTGTGACTGCCCTTGGGTGGGCCCTGACTGTTCCCATGGCAACA
2600      2610      2620      2630      2640      2650      2660

2990      3000      3010      3020      3030      3040      3050
Hum.  CTGTCTCTGTGATCTGCACAGGAAGCCTGACCCAGCCACTGTTTCCATGCCCTCGCAAATGTATCTGACCC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  CAGCCTCTGTGATCTGCTCAGGAAACCAACACCCAGGTGCTGCCCCAGTGCAACGACTTCTCTGTCTCAACC
2670      2680      2690      2700      2710      2720      2730

```

Fig. 2Qxi

```

3060      3070      3080      3090      3100      3110      3120
Hum.  ATATTGCTGCAGTTCAGAGGGCAGTGCTTTGATCTGTAGAGGACAAACGGCTCCGCCCTAGTGGAT
      .  :::::  :::::  :::::  :::::  :::::  :::::
WC1   TGCAGGCTCTGCGGCCTCAGAGGAGAGTTCTCCCTACTGCTCAGACAGCAGGCGAGCTCCGCCCTGGTGGAC
      2740      2750      2760      2770      2780      2790      2800

3130      3140      3150      3160      3170      3180      3190
Hum.  GGGACAGCCGCTGTGCCGGGAGAGTAGAGATCTATCACGACGGCTTCTGGGGCACCATCTGTGATGACG
      :::::  :  :::  :::::  :::::  :::  :::  :::::  :::::  :::  :::  :::::  :::::  :
WC1   GGGGCGGTCCCTGCGGCGGAGAGTGAGATCCTTGACCAAGGCTCCTGGGGCACCATCTGTGATGATG
      2810      2820      2830      2840      2850      2860      2870

3200      3210      3220      3230      3240      3250      3260
Hum.  GCTGGACCTGAGCGATGCCACCGTGGTGTGTCAAAGCTGGGCTGTGGAGTGGCCTTCAATGCCACGGT
      :::::  :::::  :::::  :::::  :::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
WC1   ACTGGGACCTGGACGATGCCCCGTGTGGTGTGCAGGCAGCTGGGCTGTGGAGAAGCCCTCAATGCCACGGG
      2880      2890      2900      2910      2920      2930      2940

3270      3280      3290      3300      3310      3320      3330
Hum.  CTCTGCTCACTTTGGGAGGGGTCAAGGCCCATCTGGCTGGATGACCTGAACCTGCACAGGAACGGAGTCC
      :::::  :::::  :::::  :::::  :::::  :::::  :::::
WC1   GTCTGCTCACTTCGGGGCAGGATCAGGGCCCATCTGGCTGGACGACCTGAACCTGCACAGGAAGGAGTCC
      2950      2960      2970      2980      2990      3000      3010

```

Fig. 2Qxiii

```

3340      3350      3360      3370      3380      3390      3400
Hum.  CACTTGTGCAGTGGCCCTTCCCGCGGCTGGGGGCAGCAGCTGCAGGCACAAGGAGGACGCAGGGGTCA
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1  CACGTGTGAGGTGGCCCTTCCCGGGGCTGGGGCGGCACGACTGCAGACACACAAGGAGGACGCCGGGTCA
3020      3030      3040      3050      3060      3070      3080

3410      3420      3430      3440      3450      3460      3470
Hum.  TCTGCTCAGAATTACAGCCCTTGAGGCTCTACAGTGAAACTGAAACAGAGAGCTGTGCTGGGAGATTGGA
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1  TCTGCTCAGAGTTCCTGGCCCTCAGGAT----GGTGAG-CGAGGACCAAGCAG-TGTGCTGGGTGGCTGGA
3090      3100      3110      3120      3130      3140

3480      3490      3500      3510      3520      3530      3540
Hum.  AGTCTTCTATAACGGGACCTGGGGCAGCGTCGGCAGGAGGAACATCACACAGCCATAGCAGGCATTGTG
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1  GGTTTCTACAACGGGACCTGGGGCAGTGTCTGCCGCGAGCCCCCATGGAAGATATCACTGTGTCGGTGATC
3150      3160      3170      3180      3190      3200      3210

3550      3560      3570      3580      3590      3600
Hum.  TGCAGGCAGCTGGGCTGTGGGAGAAATGGAGTTGTACGCTCGCCCCCTTA--TCT-AAGACAGGCTCTG
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1  TGCAGACAGCTTGGATGTGGGGACAGTGGA--AGTCT-CAACACCTCTGTGGTCTCAGGGAAGGTTCTA
3220      3230      3240      3250      3260      3270      3280

```

Fig. 2Qⁱⁱⁱ


```

3610      3620      3630      3640      3650      3660      3670
Hum.  GTTTCATGTGGGTGATGACATTCAAGTGTCTAAACGCATATCTCCATATGGCAGTGCCTGTCTGCCCC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GACCCCGGTGGTAGATTAAATTCAGTGTCTCGGAAATGGATAACCTCTCTCTGGCAGTGTCTTCTGGCCC
3290      3300      3310      3320      3330      3340      3350

3680      3690      3700      3710      3720      3730      3740
Hum.  ATGGAGCGGAAGAAATCTCCAGCCCCAGCAGAGACCTTGGATCACATGTGAAGATAGAATA---AGAG-
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  ATGGAATAACAGTTCATGCTCTCCAAAGGAGGAGCCTACATCTCATGTGAAGGAAGAACCCCAAGAGC
3360      3370      3380      3390      3400      3410      3420

Hum.  -----TGC-----
      : : :
WC1  TGTCCAACTGCTGCCGCTGCACACAGACAGAGAAGCTCCGCCCTCAGGGGAGGAGACAGCGAGTGTCTCAG
3430      3440      3450      3460      3470      3480      3490

3770      3780      3790      3800      3810      3820      3830
Hum.  GGAGAGTGGAGATCTGGCACGCAGGCTCCTGGGCACAGTGTGTGATGACTCCTGGACCTGGCCGAGGC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GCGGGTGGAGGTGTGGCACAAACGGCTCCTGGGGCACCGTGTGCGATGACTCCTGGAGCCTGGCAGAGGC
3500      3510      3520      3530      3540      3550      3560

```

Fig. 2Qxiv

Fig. 2Qxv

Hum.	4100	4110	4120	4130	4140
	-----TATCTT-----TGGGCTC-CTTCTC-----CTGGTTCT-----GTTTATTCTATTCTCA				
	:	:	:	:	:
	:	:	:	:	:
WC1	GGGGTTCTCTGCCTTATCCTGGGGTCGCTTCTCTTCTGGTCCTCGTCATCCTGGTGACTCAGCTACTCA				
	3850	3860	3870	3880	3890
				3900	3910
Hum.	4150	4160	4170	4180	
	CGTGGTG--CCGAGTTCAGAAACAAACATCT-----GCCC---CT---CAGAGTTT-----				
	:	:	:	:	:
	:	:	:	:	:
WC1	GATGGAGACAGAGCGCAGAGCCTTATCCAGCTATGAAGATGCTCTTGCTGAAGCTGTGTATGAGGAGCT				
	3920	3930	3940	3950	3960
				3970	3980
Hum.	4190	4200	4210	4220	
	-----CAAC-----CAGAAGGAGG---GTTCT-CTCG---AGGAGAATTATTCCATGA-----				
	:	:	:	:	:
	:	:	:	:	:
WC1	CGATTACCTTCTGACACAGAAGGAAGTCTGGGCAGCCCAGATCAGATGACTGATGTCCCTGATGAAAT				
	3990	4000	4010	4020	4030
				4040	4050
Hum.	4230	4240	4250		
	---GATGGAG-----ACCTG-----CCTC-----AAGAGAGAGGAC				
	:	:	:	:	:
	:	:	:	:	:
WC1	TATGATGATGCTGAAGAAGTACCAGTGCCCTGGAACTCCTTCTCCCTCTCAGGGGAATGAGGAGGAAGTGC				
	4060	4070	4080	4090	4100
				4110	4120

Fig. 2Qxvi

```

4260      4270      4280      4290
Hum.  CCACATGGGACAAGAAC-----CTCAGA-TGACAC---CC-----CCAA-----
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1   CCCCAGAGAAGGAGGACGGGGTGAGGTCCTCTCAGACAGGCTCTTCTGAACTTCTCCAGAGGCAGC
4130      4140      4150      4160      4170      4180      4190

      4300      4310      4320      4330
Hum.  ----CCATGGTT--GTGAAGA-----TGCTAGCGACAC-----ATCGCTG--TTGGGAGTT
      :: :: . :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1   TAATCCTGGGAAGGAGAAGAGAGCTTCTGGCTGCTCCAGGGGAAGAAAGGGGATGCTGGGTATGATGAT
4200      4210      4220      4230      4240      4250      4260

      4340      4350
Hum.  CTT-----CCTG-----CCTCTGAAGCCACAAA
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1   GTTGAAC TCAGTGCCCTGGGGAACATCCCCAGTGACTTTCTCG
4270      4280      4290      4300

```

Fig. 2Qxviii

GTCGACCCACGCGTCCGGTCTGTGGCTGAGC	ATG	GCC	CTC	CCA	GCC	CTG	GGC	CTG	GGC	CTG	GAC	CCC	TGG	S	12					
L	L	G	L	F	L	F	Q	L	L	Q	L	L	P	T	A	G	32			
CTC	CTG	GGC	CTT	TTC	CTC	TTC	CAA	CTG	CTT	CAG	CTG	CTG	CCG	ACG	ACC	GGG	127			
G	G	G	Q	G	P	M	P	R	V	R	Y	Y	A	G	D	E	R	A	52	
GGA	GGC	GGG	CAG	GGG	CCC	ATG	CCC	AGG	GTC	AGA	TAC	TAT	GCA	GGG	GAT	GAA	CGT	AGG	GCA	187
L	S	F	F	H	Q	K	G	L	Q	D	F	D	T	L	L	L	S	G	D	72
CTT	AGC	TTC	TTC	CAC	CAG	AAG	GGC	CTC	CAG	GAT	TTT	GAC	ACT	CTG	CTC	CTG	AGT	GGT	GAT	247
G	N	T	L	Y	V	G	A	R	E	A	I	L	A	L	D	I	Q	D	P	92
GGA	AAT	ACT	CTC	TAC	TAC	GTG	GGG	GCT	CGA	GAA	GCC	ATT	CTG	GCC	TTG	GAT	ATC	CAG	GAT	307
G	V	P	R	L	K	N	M	I	P	W	P	A	S	D	R	K	K	S	E	112
GGG	GTC	CCC	AGG	CTA	AAG	AAC	ATG	ATA	CCG	TGG	CCA	GCC	AGT	GAC	AGA	AAA	AAG	AGT	GAA	367
C	A	F	K	K	K	S	N	E	T	Q	C	F	N	F	I	R	V	L	V	132
TGT	GCC	TTT	AAG	AAG	AAG	AGC	AAT	GAG	ACA	CAG	TGT	TTC	AAC	TTC	ATC	CGT	GTC	CTG	GTT	427
S	Y	N	V	T	H	L	Y	T	C	G	T	F	A	F	S	P	A	C	T	152
TCT	TAC	AAT	GTC	ACC	CAT	CTC	TAC	ACC	TGC	GGC	ACC	TTC	GCC	TTC	AGC	CCT	GCT	TGT	ACC	487
F	I	E	L	Q	D	S	Y	L	L	P	I	S	E	D	K	V	M	E	G	172
TTC	ATT	GAA	CTT	CAA	GAT	TCC	TAC	CTG	TTG	CCC	ATC	TCG	GAG	GAC	AAG	GTC	ATG	GAG	GGA	547

Fig. 3A

K G Q S P F D P A H K H T A V L V D G M 192
 AAA GGC CAA AGC CCC TTT GAC CCC GCT CAC AAG CAT ACG GCT GTC TTG GTG GAT GGG ATG 607

 L Y S G T M N N F L G S E P I L M R T L 212
 CTC TAT TCT GGT ACT ATG AAC AAC TTC CTG GGC AGT GAG CCC ATC CTG ATG CGC ACA CTG 667

 G S Q P V L K T D N F L R L H H D A S 232
 GGA TCC CAG CCT GTC CTC AAG ACC GAC AAC TTC CTC CGC TGG CTG CAT CAT GAC GCC TCC 727

 F V A A I P S T Q V V Y F F E E T A S 252
 TTT GTG GCA GCC ATC CCT TCG ACC CAG GTC GTC TAC TTC TTC TTT GAG GAG ACA GCC AGC 787

 E F D F F E R L H T S R V A R V C K N D 272
 GAG TTT GAC TTC TTT GAG AGG CTC CAC ACA TCG CGG GTG GCT AGA GTC TGC AAG AAT GAC 847

 V G G E K L L Q K K W T T F L K A Q L L 292
 GTG GGC GGC GAA AAG CTG CTG CAG AAG AAG TGG ACC ACC TTC CTG AAG GCC CAG CTG CTC 907

 C T Q P G Q L P F N V I R H A V L L P A 312
 TGC ACC CAG CCG GGC CAG CTG CCC TTC AAC GTC ATC CGC CAC GCG GTC CTG CTC CCC GCC 967

 D S P T A P H I Y A V F T S Q W Q V G G 332
 GAT TCT CCC ACA GCT CCC CAC ATC TAC GCA GTC TTC ACC TTC CAG TGG CAG GTT GGC GGC 1027

 T R S S A V C A F S L L D I E R V F K G 352
 ACC AGG AGC TCT GCG GTT TGT GCC TTC TCT CTC TTG GAC ATT GAA CGT GTC TTT AAG GGC 1087

46/95

Fig. 3B

K Y K E L N K E T S R W T T Y R G P E T 372
 AAA TAC AAA GAG TTG AAC AAA GAA ACT TCA CGC TGG ACT ACT TAT AGG GGC CCT GAG ACC 1147

 N P R P G S C S V G P S S D K A L T F M 392
 AAC CCC CGG CCA GGC AGT TGC TCA GTG GGC CCC TCC TCT GAT AAG GCC CTG ACC TTC ATG 1207

 K D H F L M D E Q V V G T P L L V K S G 412
 AAG GAC CAT TTC CTG ATG ATG GAT GAG CAA GTG GTG GGC ACG CCC CTG CTG GTG AAA TCT GGC 1267

 V E Y T R L A A V E T A Q G L D G H S H L 432
 GTG GAG TAT ACA CGG CTT GCA GTG GAG ACA GCC CAG GGC CTT GAT GGG CAC AGC CAT CTT 1327

 V M Y L G T T T G S L H K A V V S G D S 452
 GTC ATG TAC CTG GGA ACC ACC ACA GGG TCG CTC CAC AAG GCT GTG GTA AGT GGG GAC AGC 1387

 S A H L V E E I Q L F P D P E P V R N L 472
 AGT GCT CAT CTG GTG GAA GAG ATT CAG CTG TTC CCT GAC CCT GAA CCT GTT CGC AAC CTG 1447

 Q L A P T Q G A V F V G F S G G V W R V 492
 CAG CTG GCC CCC ACC CAG GGT GCA GTG TTT GTA GGC TTC TCA GGA GGT GTC TGG AGG GTG 1507

 P R A N C S V Y E S C V D C V L A R D P 512
 CCC CGA GCC AAC TGT AGT GTC TAT GAG AGC TGT GTG GAC TGT GTC CTT GCC CGG GAC CCC 1567

 H C A W D P E S R T C C L L S A P N L N 532
 CAC TGT GCC TGG GAC CCT GAG TCC CGA ACC TGT TGC CTC CTG TCT GCC CCC AAC CTG AAC 1627

47/95

Fig. 3C

S W K Q D M E R G N P E W A C A S G P M 552
TCC TGG AAG CAG GAC ATG GAG CGG GGG AAC CCA GAG TGG GCA TGT GCC AGT GGC CCC ATG 1687

S R S L R P Q S R P Q I I K E V L A V P 572
AGC AGG AGC CTT CGG CCT CAG AGC CGC CCG CAA ATC ATT AAA GAA GTC CTG GCT GTC CCC 1747

N S I L E L P C P H L S A L A S Y Y W S 592
AAC TCC ATC CTG GAG CTC CCC TGC CCC CAC CTG TCA GCC TTG GCC TCT TAT TAT TGG AGT 1807

H G P A A V P E A S S T V Y N G S L L L 612
CAT GGC CCA GCA GTC CCA GAA GCC TCT TCC ACT GTC TAC AAT GGC TCC CTC TTG CTG 1867

I V Q D G V G G L Y Q C W A T E N G F S 632
ATA GTG CAG GAT GGA GTT GGG GGT CTC TAC CAG TGC TGG GCA ACT GAG AAT GGC TTT TCA 1927

Y P V I S Y W V D S Q Q CAG GAC GAC CAG ACC CTG GCC CTG GAT CCT GAA 1987
TAC CCT GTG ATC TCC TAC TGG GTG GAC GAC AGC CAG GTG AAG GTC CCG TTG ACC AGG GTC AGT GGT GGC GCC 2047

L A G I P R E H V K V P L T R V S G A 672
CTG GCA GGC ATC CCC CGG GAG CAT GTG AAG GTC CCG TTG ACC AGG GTC AGT GGT GGC GCC 2047

A L A A Q Q S Y W P H F V T V T V L F A 692
GCC CTG GCT GCC CAG CAG TCC TAC TGG CCC CAC TTT GTC ACT GTC ACT GTC CTC TTT GCC 2107

L V L S G A L I I L V A S P L R A L R A 712
TTA GTG CTT TCA GGA GCC CTC ATC ATC GTG GCC TCC CCA TTG AGA GCA CTC CGG GCT 2167

Fig. 3D

R G K V Q G C E T L R P G G E K A P L S R 732
CGG GGC AAG GTT CAG GGC TGT GAG ACC CTG CGC CCT GGG GAG AAG GCC CCG TTA AGC AGA 2227

E Q H L Q S P K E C R T S A S D V D A D 752
GAG CAA CAC CTC CAG TCT CCC AAG GAA TGC AGG ACC TCT GCC AGT GAT GTG GAC GCT GAC 2287

N N C L G T E V A * 762
AAC AAC TGC CTA GGC ACT GAG GTA GCT TAA 2317

ACTTAGGCACAGCCGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGCGGCCAAGCACAGCCCTGACTAGGA 2396
TGACAGCAGCACAAAGACACCTTTCTCCCTGAGAGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGG 2475
TGATGCACAGCAGTCTGCCCTCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGCTACCC 2554
CCAGACCTGCTCCTACACTGATATTGAAGAACCCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGACCCCTCCAGAAA 2633
CACAGTGTTCAGAGATCCTAAAAAACCTGCCCTGTCCAGGACCCCTATGGTAATGAACACCAACATCTAAACAATC 2712
ATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCA 2791
TGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCCGCTGACTCCCAGGAAGTCTTTCTCTGAAGTCTGACC 2870
ACCTTCTTCTTGTTCAGTTGGGCAGACTCTGATCCCTTCTGCCCTGGCAGATGGCAGGGTAATCTGAGCCTTCT 2949
TCACTCCTTTACCCCTAGCTGACCCCTTCACTCTCCCTCCCTTTTCTCTTTTGGGATTCAGAAAACTGCTTGTG 3028
AGAGACTGTTTATTTTATTAAATAATATAAGGCTTAAAAAATAAAAAAAGGGCGGCCG 3104

Fig. 3E

Hum.	10	20	30	40	50	60	70
	MALPALGLDPWSLLGLFLFQLLQLLP	TTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQDFD	LLLL				
	:	:
Mur.	10	20	30	40	50	60	70
	MALPSLGQDSWSLLRVFFQFLFLLPSLP	PASGTGGQGPMPRVKYHAGDGHRA	LSFFQKGLRDFD	LLLL			

Hum.	80	90	100	110	120	130	140
	GDGNTLYVGAREAILALDIQDP	GVPR	LKNMIPWASDRKKSECAFKKKS	NETQC	FN	FIRLVSYNV	THLY

Mur.	80	90	100	110	120	130	140
	DDGNTLYVGARETVLALNIQNP	GI	PR	LKNMIPWASERKKTECAFKKKS	NETQC	FN	FIRLVSYNATHLY

Hum.	150	160	170	180	190	200	210
	TCGTFAFSPACTFIELQDSYLL	PISEDKVMEGKGQSP	FDPAHKHTAVLVDG	MLYSGTMN	FLGSE	PILMR	

Mur.	150	160	170	180	190	200	210
	ACGTFAFSPACTFIELQDSLL	PILIDKVM	DGKGQSP	LTFTSTQAVLVDG	MLYSGTMN	FLGSE	PILMR

Hum.	220	230	240	250	260	270	280
	TLGSQPVLKTDN	FLRWLHHDAS	FVA	AI	PSTQVVYFFFEET	ASE	DFDFFERLH

Mur.	220	230	240	250	260	270	280
	TLGSHPV	LKTDIFLRWLHAD	AS	FVA	AI	PSTQVVYFFFEET	ASE

Fig. 3F

Hum.	290	300	310	320	330	340	350
	KKWTTFLKAQLLCTQPGQLPENVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVF						
Mur.	290	300	310	320	330	340	350
	KKWTTFLKAQLLCAQPGQLPFIIRHAVLLPADSPSVSRIYAVFTSQWQVGGTRSSAVCAFSLLDIERVF						
Hum.	360	370	380	390	400	410	420
	KGKYKELNKETSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV						
Mur.	360	370	380	390	400	410	420
	KGKYKELNKETSRWTTYRGSEVSPRPGSCSMGPSSDKALTFMKDHFLMDEHVVGTPLLVKSGVEYTRLAV						
Hum.	430	440	450	460	470	480	490
	ETAQGLDGHSHLVMYLGTGTLGHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGA VFGFSGGVW						
Mur.	430	440	450	460	470	480	490
	ESARGLDGSSHVMYLGSTGTGTLGHKAVVPQDSSAYLVEEIQLSPDSEPVNRNLQLAPAQGA VFAFGSGGIW						
Hum.	500	510	520	530	540	550	560
	RVPRANC SVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLSWKQDMERGNPEWACASGPM SRSRLRPQS						
Mur.	500	510	520	530	540	550	560
	RVPRANC SVYESCVDCVLARDPHCAWDPESTRCLSLSGST-KPWKQDMERGNPEWVCTRGPMARS PRRQS						

Fig. 3G

Hum.	570	580	590	600	610	620	630
	RPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLI	VQDGVGGLYQCWATENG					
Mur.	560	570	580	590	600	610	620
	PPQIIKEVLTVPNSILELPCPHLSALASYWSHGRAKISEASATVYNGSLLLLPQDGVGGLYQCVATENG						
Hum.	640	650	660	670	680	690	700
	FSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVT	TVL	FALVLSGALI				
Mur.	630	640	650	660	670	680	690
	YSYPVVSYWVDSQDQPLALDPELAGVPRERVQVPLTRVGGGASMAAQRSYWPHFLI	VTVLLAIVLLGVLT					
Hum.	710	720	730	740	750	760	
	ILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASD	VDADNNCLGTEVA					
Mur.	700	710	720	730	740	750	760
	LLASPLGALRARGKVQCGMLPPREKAPLSRDQHLQPSKDHR	TSASD	VDADNNHLGAEVA				

Fig. 3H

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Hum.  GTCG-AC-CC-----ACG-----CGTCCGGT-----CTGTGGCTGAGCATGGC
      :: :: ::
Mur.  CTCGACGCCCTGGGTTAGGGTCTGTACTGCTGGGAACCATCTGGTGACCATCTCAGGCTGACCATGGC
      10   20   30   40   50   60   70

Hum.  CCTCCAGCCCTGGGCTGGACCCCTGGAGCCTCCTGGGCCCTTTCCCTCTTCCAACCTGCTTC-AGCTGCT
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Mur.  CCTACCATCCCTGGGCCAGGACTCATGGAGTCTCCTGCGTGTTTTTCTTCCAACCT-CTTCCTGCTGCC
      80   90   100  110  120  130

Hum.  GCTGCCGACGACCGCGGGGGAGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGAT
      110  120  130  140  150  160  170
Mur.  ATCACTGCCACCTGCTTCTGTGGACTGGTGGTCAGGGGCCCATGCCCAGAGTCAAATACCATGCTGGAGAC
      140  150  160  170  180  190  200

Hum.  GAACGTAGGGCACTTAGCTTCTTCCACCAGAAAGGCCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTG
      180  190  200  210  220  230  240
Mur.  GGGCACAGGGCCCTCAGCTTCTTCCAACAAAGGCCCTCCGAGACTTTGACACGCTGCTCCTGAGTGACG
      210  220  230  240  250  260  270

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Fig. 3I

Fig. 3J

Hum.	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830
	GGAGGACAAGGTCATGGAGGAAAGGCCAAAGCCCTTTGACCCCGCTCACAAGCATACG-GCTGTCTT																														

Mur.	GATAGACAAGGTCATGGACGGGAAGGCCAAAGCCC-TTTGACCCCTGTTCAAGCACACAAAGCTGTCTT																														
	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860
Hum.	GGTGGATGGGATGCTCTATTCTGTACTATGAACAACCTTCTTGGCAGTGAGCCCATCCTGATGCGCACACA																														

Mur.	GGTCGATGGGATGCTTTATTCCGGCACCATGAACAACCTTCTTGGCAGCGAGCCCATCCTGATGCGGACACA																														
	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930
Hum.	CTGGGATCCCAGCCTGTCTCAAGACCGACAACCTTCTCCGCTGGCTGCATCATGACGCCCTCCTTTGTGG																														

Mur.	CTGGGATCCCATCCTGTCTCAAGACTGACATCTTCTTACGCTGGCTGCACGGGATGCCCTCCTTCGTGG																														
	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000
Hum.	CAGCCATCCCCTTCGACCCAGGTCGTCTACTTCTTCTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGA																														

Mur.	CAGCCATTCCATCCACCCAGGTCGTCTATTCTTCTTTGAGGAGACAGCCAGCGAGTTTGACTTCTTTGA																														
	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040	1050	1060	1070

Fig. 3K

	810	820	830	840	850	860	870
Hum.	GAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAAATGACGTGGGCGGCGGAAAAGCTGCTGCAGAAG						
	840	850	860	870	880	890	900
Mur.	AGAGCTGTATATATCCAGGGTGGCTCAAGTCTGCAAGAACGACGTGGGCGGTGAAAAGCTGCTGCAGAAG						
	880	890	900	910	920	930	940
Hum.	AAGTGGACCACCTTCCTGAAGGCCAGCTGCTGCACCCAGCCGGGCGAGCTGCCCTTCAACGTCATCC						
	910	920	930	940	950	960	970
Mur.	AAGTGGACCACCTTCCTCAAAGCCCCAGTTGCTCTGCGCTCAGCCAGGCGAGCTGCCATTCAACATCATCC						
	950	960	970	980	990	1000	1010
Hum.	GCCACGGGTCCTGCTCCCCCGCGATTCTCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTG						
	980	990	1000	1010	1020	1030	1040
Mur.	GCCACGGGTCCTGCTGCCCGCGGATTCTCCCTCTGTTCCTCCGCATCTACGCAGTCTTTACCTCCCAGTG						
	1020	1030	1040	1050	1060	1070	1080
Hum.	GCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAG						
	1050	1060	1070	1080	1090	1100	1110
Mur.	GCAGGTTGGCGGGACCAGGAGCTCAGCAGTCTGTGCGCTTCTCTCTCAGCGACATTGAGCGAGTCTTTAA						

Fig. 3L


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1090      1100      1110      1120      1130      1140      1150
Hum.  GGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGCCCTGAGACCAACCCCC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  GGGAGTACAAGGAGCTGAACAAGGAGACCTCCCGCTGGACCACTTACCGGGGCTCAGAGGTCAGCCCCGA
1120      1130      1140      1150      1160      1170      1180

1160      1170      1180      1190      1200      1210      1220
Hum.  GGCCAGGCAGTTGCTCAGTGGGCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCTGAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  GGCCAGGCAGTTGCTCCATGGGCCCTCCTCTGACAAAGCCTTGACCTTCATGAAGGACCATTTTCTGAT
1190      1200      1210      1220      1230      1240      1250

1230      1240      1250      1260      1270      1280      1290
Hum.  GGATGAGCAAGTGGTGGGACGCCCTGCTGGTGAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  GGATGAGCACGTGGTAGGAACACCCCTGCTGGTGAAGTCTGGTGTGGAGTACACACGGCTTGTGTGGAG
1260      1270      1280      1290      1300      1310      1320

1300      1310      1320      1330      1340      1350      1360
Hum.  ACAGCCCAGGGCCTTGATGGGCACAGCCCATCTTGTTCATGTACCTGGGAACCAACACAGGGTCGCTCCACA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  TCAGTCGGGGCCTTGATGGAGCAGCCATGTGGTCAATGTATCTGGGTACCTCCACGGGTCCCCTGCACA
1330      1340      1350      1360      1370      1380      1390

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Fig. 3M

	1370	1380	1390	1400	1410	1420	1430
Hum.	AGGCTGTGGTAAGTGGGGACAGCAGTGTCTCATCTGGTGGAGAGATT	CAGCTGTTCCCTGACCCCTGAACC					
	1400	1410	1420	1430	1440	1450	1460
Mur.	AGGCTGTGGTGCCTCAGGACAGCAGTGTATCTCGTGGAGGAGATT	CAGCTGAGCCCTGACTCTGAGCC					
	1470	1480	1490	1500	1510	1520	1530
Hum.	TGTTTCGAAACCTGCAGCTGGCCCCCACCAGGGTG	CAGTGTTCAGGCTTCTCAGGAGGTCTGGAGG					
	1540	1550	1560	1570	1580	1590	1600
Mur.	TGTTTCGAAACCTGCAGCTGGCCCCCAGGGTG	CAGTGTTCAGGCTTCTCAGGAGGTCTCAGGAGGTCTGGAGG					
	1610	1620	1630	1640	1650	1660	1670
Hum.	CCTGGGACCCCTGAGTCCC	GAAACCTGTTGCCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACAT					
	1680	1690	1700	1710	1720	1730	1740
Mur.	CCTGGGACCCCTGAAATCAAGACTCTGCAGCCTTCTGTCTGGCTC-TACCAAGCCT--TGGAAGCAGGACAT						

Fig. 3N

	1650	1660	1670	1680	1690	1700	1710
Hum.	GGAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCCATGAGCAGGAGCCTTCGGCCCTCAGAGCCGC						
	1680	1690	1700	1710	1720	1730	1740
Mur.	GGAACGCGGCAACCCGGAGTGGGTATGCACCCCGTGGCCCCCATGGCCAGGAGCCCCCGGCGTCAAGAGCCCC						
	1720	1730	1740	1750	1760	1770	1780
Hum.	CCGCAATCATTAAGAAGTCCTGGCTGTCCCAACTCCATCCTGGAGCTCCCTGCCCCACCTGTCTCAG						
	1750	1760	1770	1780	1790	1800	1810
Mur.	CCTCAACTAATTAAGAAGTCCTGACAGTCCCCCAACTCCATCCTGGAGCTGGCGTGGCCCCCACCTGTCTCAG						
	1790	1800	1810	1820	1830	1840	1850
Hum.	CCTTGGCCCTCTTATTATTGGAGTCATGGCCCCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGG						
	1820	1830	1840	1850	1860	1870	1880
Mur.	CACTGGCCCTCTTACCACCTGGAGTCATGGCCGAGCCAAATCTCAGAAGCCTCTGCTACCGTCTACAATGG						
	1860	1870	1880	1890	1900	1910	1920
Hum.	CTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGTGGGCAACTGAGAATGGCTTT						
	1890	1900	1910	1920	1930	1940	1950
Mur.	CTCCCTCTTGCTGCTGCCGAGGATGGTGTCTGGGGGCTCTACCAGTGTGTGGCGACTGAGAACGGCTAC						

Fig. 30

	1930	1940	1950	1960	1970	1980	1990
Hum.	TCATACCCCTGTGATCTCCTACTGGGTGGACAGCCAGGACACCCCTGGCCCTGGATCCTGAACTGGCAG						
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
Mur.	TCATACCCCTGTGGTCTCCTATTGGGTAGACAGCCAGGACACCCCTGGCGCTGGACCCCTGAGCTGGCGG						
	1960	1970	1980	1990	2000	2010	2020
	2000	2010	2020	2030	2040	2050	2060
Hum.	GCATCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGCGCCCTGGCTGCCAGCA						
	::::	::::	::::	::::	::::	::::	::::
Mur.	GCGTTCCCCGTGAGCGTGTGCAGGTCCCGCTGACCAGGGTCGGAGGGAGCTTCCATGGCTGCCACGCG						
	2030	2040	2050	2060	2070	2080	2090
	2070	2080	2090	2100	2110	2120	2130
Hum.	GTCCTACTGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCCTTAGTGCTTTCAGAGCCCTCATCATC						
	::::::::::	::::	::::	::::	::::	::::	::::
Mur.	GTCCTACTGGCCCCCATTTTCTCATCGTTACCGTCCCTCCTGGCCATCGTGCTCCTGGGAGTGCTCACTCTC						
	2100	2110	2120	2130	2140	2150	2160
	2140	2150	2160	2170	2180	2190	2200
Hum.	CTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAAGGCTGTGAGACCCCTGCGCCCTG						
	::	:	:	:	:	:	:
Mur.	CTCCTCGCTTCCCCACTGGGGCGCTCGGGGCTCGGGGTAAGGTTCAAGGCTGTGGATGCTGCCCCCA						
	2170	2180	2190	2200	2210	2220	2230

Fig. 3P

Hum.	GGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGA	2210	2220	2230	2240	2250	2260	2270
Mur.	GGGAAAAGGCTCCACTGAGCAGGAGCACACCTCCAGCCCTCCAAGGACCACAGGACCTCTGCCAGTGA	2240	2250	2260	2270	2280	2290	2300
Hum.	TGTGGACGCTGACAACTGCCTAGGCACCTGAGGTAGCTTAAACTCTAGGCACAGG-CCGGGGCTG--C	2280	2290	2300	2310	2320	2330	2340
Mur.	CGTAGATGCCGACAAACAACCATCTGGCGCGCCGAAGTGGCTTAAACA-GGGACACAGATCCGCAGCTGAGC	2310	2320	2330	2340	2350	2360	2370
Hum.	GGTGCAGGCACCTGGCCATGCTGGCTGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAA	2350	2360	2370	2380	2390	2400	2410
Mur.	AGAGCAAGCCACTGGCCTTGTGGCTATGC---CAGGCACAG-----TGCCACTCT--	2380	2390	2400	2410	2420		
Hum.	AGACCACCTTTCTCCCCCTGAGAGGAGCTTCTGTCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGC	2420	2430	2440	2450	2460	2470	2480
Mur.	-GACCA-----GGTAGGAG--GCT-CT-C-CTGCTA-ACGTGTGTAC-CTACAG-----C	2430	2440	2450	2460	2470	2480	

File 30

Fig. 3R

```

                2760      2770      2780      2790      2800      2810
Hum.  ----GCTGCCGCTTTGGACACCAACACTCCCTTCT-CCCAGG-GTCATGCAGGGATCTGCTCCCTCCTGC
        ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Mur.  AGCAGCTGCTGCTTTGAACACACAGCCACCCCTCCTTCCCAAGAGTCTCTATGGAGTTGGC-CCCTTGTGT
        2730      2740      2750      2760      2770      2780      2790

                2820      2830      2840      2850      2860      2870      2880
Hum.  TTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCTTCTTGC
        ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Mur.  TTCCCTTACCAGTCGGGCCATACTGTTT---GGGAAGTCATCTCTGAAGTCTAACCCACCTTCCCTTCTTGG
        2800      2810      2820      2830      2840      2850

                2890      2900      2910      2920      2930      2940      2950
Hum.  TTCAGTTGGGCAGACTCTGATCCCT---TC TGCCCTGGCAGAAATGCAGGGGTAATCTGAGCCTTCTTC
        ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Mur.  TTCAGTTTGGACAGATTGTTATTATTGTCTCTGCCCTGGCTAGAAATGGGGGCATAATCTGAGCCTTGTTTC
        2860      2870      2880      2890      2900      2910      2920

                2960      2970      2980      2990      3000      3010
Hum.  ACTCCTTTACCC---TAGCTGACCCCTTCACCTCTCCCTCCCTCCCTTTTCCCTTTGTTTGGGATTCAGA
        ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Mur.  ---CCTTGTCAGTGTGGCTGACCC-TTGACCTCTTCCCTTCCCTCC---TCCCTTTGTTTGGGATTCAGA
        2930      2940      2950      2960      2970      2980      2990

```

Fig. 3S

Fig. 3T

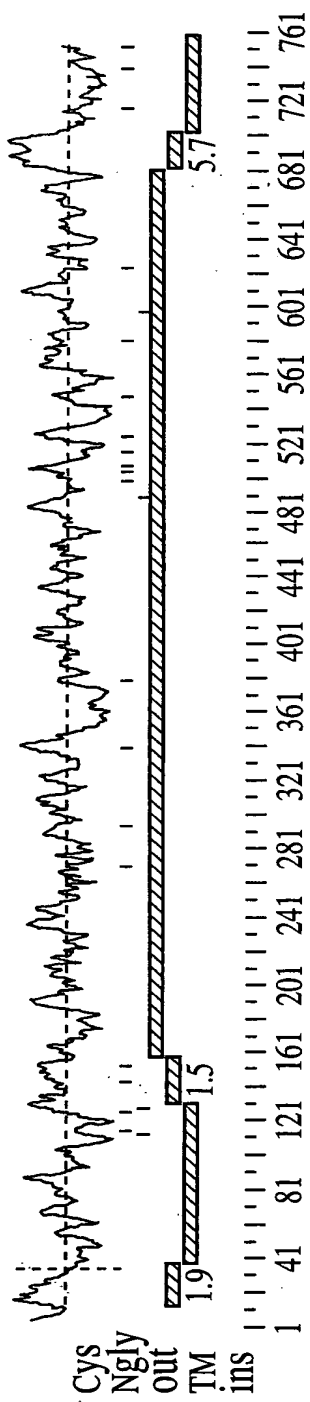


Fig. 3U

GTCGACCCACGCGTCCGCGGACGCGGTGGGACGGCTCCCGGCTGCAGTCTGCCCGCCCGCGCGGGCCGAGTC 79
 GCGAAGCGCGCCTGCGACCCGCGTCCGGCGCGCTGGAGAGACGCGAGGAGCC ATG AGG CGC CAG CCT GCG 6
 K V A A L L L G L L L E C T E A K K H C 26
 AAG GTG GCG CTG CTG CTC GGG CTG CTC TTG GAG TGC ACA GAA GCC AAA AAG CAT TGC 212
 W Y F E G L Y P T Y Y I C R S Y E D C C 46
 TGG TAT TTC GAA GGA CTC TAT CCA ACC TAT TAT ATA TGC CGC TCC TAC GAG GAC TGC TGT 272
 G S R C C V R A L S I Q R L W Y F W F L 66
 GGC TCC AGG TGC TGT GTG CGG GCC CTC TCC ATA CAG AGG CTG TGG TAC TTC TGG TTC CTT 332
 L M M G V L F C C G A G F I R R M Y 86
 CTG ATG ATG GGC GTG CTT TTC TGC TGC GGA GCC GGC TTC TTC ATC CGG AGG CGC ATG TAC 392
 P P P L I E E P A F N V S Y T R Q P P N 106
 CCC CCG CCG CTG ATC GAG GAG CCA GCC TTC AAT GTG TCC TAC ACC AGG CAG CCC CCA AAT 452
 P G P G A Q Q P G P P Y T D P G P G 126
 CCC GGC CCA GGA GCC CAG CAG CCG GCG CCG CCC TAT TAC ACT GAC CCA GGA GGA CCG GGG 512
 M N P V G N S M A M A F Q V P P N S P Q 146
 ATG AAC CCT GTC GGC AAT TCC ATG GCA ATG GCT TTC CAG GTC CCA CCC AAC TCA CCC CAG 572

66 / 95

Fig. 4A

G	S	V	A	C	P	P	P	A	Y	C	N	T	P	P	P	Y	E	166	
GGG	AGT	GTG	GCC	TGC	CCG	CCC	CCT	CCA	GCC	TAC	TGC	AAC	ACG	CCT	CCG	CCC	TAC	GAA	632

Q	V	V	K	A	K	*													173
CAG	GTA	GTG	AAG	GCC	AAG	TAG													653

TGGGGT	CCCC	CACGTG	CAAGAG	GAGACAGG	AGAGGG	CCCTTCC	CTGG	CCCTTCT	GTCTT	CTGTG	CTTCT	GTCTT	CGTT	GATGT	TCAC	TTCC	CAG	732
GAACGG	TCTCG	TGGGCTG	CTAAGG	GCAGTT	CCCTCT	GATATC	CTCAC	AGCAAG	CACAGC	TCCTCT	TTCA	GGCTT	CCATGG	811				
AGTACA	ATATG	AACTCAC	ACTTTG	TCTCCT	CTGTG	TTCTG	ACGC	AGTCTG	TGCTC	TACAT	GGTAG	TGT	890					
GGTGAC	AGTCCCC	AGGGCTG	ACGTCC	TACGG	TGGCGTG	ACCAG	ATCTA	CAGG	AGAG	ACTG	AGAG	GGAAG	AGGC	969				
TGCTG	AGGTG	CAGGTG	GCATG	AGGG	CCAGG	CCAGC	ATCC	AGCA	AGCATC	CTTCT	GCCC	GGTAT	TAAT	1048				
AAGCCC	ATGCC	GGGCTC	AGCCG	ATGA	AGCAG	CAGCC	AGCTG	AGCTG	AGCC	AGCAG	GTCTG	CTCC	AGCC	1127				
CCTCTC	GTACG	CTTCC	TAGAG	AGCTG	TGG	AGAG	ACATTC	CAGG	AGAG	CAAG	CCCC	CTTGT	CATG	1206				
CTGTT	CATATC	CTAA	AGATAG	ACTTCT	CTG	CACCC	AGGAG	CACG	TGAC	GTG	AGCTC	TAC	CGG	1285				
CTAGAA	TCAGG	CTTG	AGGCTG	ACAGT	GATCTG	ACATCC	ACTA	AGCA	AAATTT	ATTAA	ATTC	ATGG	AAATCA	1364				
CTTCCT	TGCCCC	AACTG	AGACAT	TGCA	TTTGT	GAGCTC	TGGT	CTGAT	TTGG	AGAA	AGGACTG	TAC	CCATTT	1443				
GTGTG	TTTATG	GAAAGT	GCATG	AGCG	TCC	TGG	CTTGA	AAATC	AGACTG	GGTGT	GTCTT	CCC	TGG	1522				
CTCTC	AGGCA	TTCTC	AGGCC	CGGGT	CTCCT	CCCTC	AGG	CAGCTC	CCAGT	GGTCT	TGA	AGG	TGCTT	1601				
ACGGG	CACATC	TGGCTG	GGAAGT	CACATG	GACTCT	TCC	AGG	AGAG	AGAC	CAGCTG	AGCG	GTCTC	CTG	1680				
GTTGGG	TCTA	AGCGG	TGTGT	CTGG	CTCCA	AGG	AGG	AGCTT	GCTGG	AAA	AGAC	AGG	AACTG	1759				
TGCAC	TGAC	CATG	TTGT	CAATA	TTAGA	ATAA	AGAA	AGTGT	CGG	AAATG	CACAT	TCC	TGG	1838				
CCCC	AGGATC	TCAC	AGGTAG	TCCTC	CTG	AGTGT	GACG	GTAG	CGGG	AGCTAG	TTCC	CGC	CAATAG	1917				
TGTGT	GAA	CGCTG	ACCTG	TCTGT	GCTAA	GAGCTA	TGC	AGCTT	AGCTG	AGG	CGCCTAG	ATTAC	TAG	1996				
CACGGG	AAATG	AGGTG	GGGTG	CTTAT	TTTTT	TAATG	AACTA	ATC	AG	CCCTC	TTG	AG	AAATG	2075				
AGCAT	CAAG	ACATC	TCATG	GGAAGT	GGATAC	GGAGT	GATTTG	GTG	TCC	ATGCTTT	TCA	CTC	TG	2154				

Fig. 4B

AACCTCCTGGGGAATTTGTGGGAGACACTTGGGAACAAAACAGACACCCCTGGGAATGCAGTTGCAAGCACAGATGCTG 2233
CCACCAGTGTCTGTGACCAACCTGGTGTGACTGCTGACTGCCAGCGTGGTACCTCCCATGCTGCAGGCCCTCCATCTAAA 2312
TGAGACAAACAAGCACAAATGTTCACTGTTTACAACCAAGACAACACTGCGTGGTCCAAACACTCCTCTTCTCCAGGTCA 2391
TTTGTTTTGCATTTTAAATGCTTTTATTTTGTAAATGAAAAGCACACTAAGCTGCCCTGGAATCGGGTGCAGCTGA 2470
ATAGGCACCCAAAAGTCCGTGACTAAATTTTCGTTTGTCTTTTGTATAGCAAAATATGTTAAGACACAGTATGGCTAGG 2549
GCTCAACAAATTTTGATTTCCCATGTTTGTGTGAGACAGAGTTTGTTTTCCCTTGAACTTGGTTAGAAATTGTGCTACTGT 2628
GAACGCTGATCCTGCATATGGAAGTCCCACTTTGGTGACATTTTCTGGCCATTTCTTGTTCATTGTGTGGATGGTGG 2707
TTGTGCCCCACTTCCCTGGAGTGAGACAGCTCCCTGGTGTAGAAATCCCGGAGCGTCCGTTGTTTGTGATAGGATCCTGTTTCCCT 2786
CAGATCTGTGCAATGCTTTTCCCTGCAACAAATTGGCTCGTTTCTCTTTTGTGTTTGTGATAGGATCCTGTTTCCCT 2865
ATGTGTGCAAAATAAAATAAATTTGGGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2944
AAAAAAAAAAGGGGCGCGC

Fig. 4C

GTCGACCCACGCGTCCGGCCGGCGGTCTTCTGCGGGCTTCAGCTCGTATCCCCGGAGTCCACCCGCCGTCGCCGGGT 79

GCGGACTGGCCCTGAGCTGGCCGTACAGCCCGGCTTCGGACGGTCTCGCTGGAGCC ATG GGC CGC CGG CTC 151

M G R R L 5

G R V A A L L L G L L V E C T E A K K H 25
GGC AGG GTG GCG GCG CTG CTC GGG CTG CTA GTG GAG TGC ACT GAG GCC AAA AAA CAT 211

Fig. 4D

C W Y F E G L Y P T Y Y I C R S Y E D C 45
 TGC TGG TAT TTT GAA GGA CTC TAT CCC ACA TAC TAT ATA TGC CGT TCC TAT GAA GAC TGC 271

 C G S R C C V R A L S I Q R L W Y F W F 65
 TGT GGC TCC AGG TGC TGT GTG AGG GCC CTT TCC ATA CAG AGG CTG TGG TAT TTT TGG TTC 331

 L L M M G V L F C C G A G F I R R R M 85
 CTG CTG ATG ATG GGT GTG CTG TTC TGC TGT GGT GCC GGT TTC ATT CGC CGG CGC ATG 391

 Y P P P L I E E P T F N V S Y T R Q P P 105
 TAT CCG CCA CCA CTC ATT GAG GAG CCC ACA TTC AAT GTG TCC TAT ACC AGG CAG CCA CCA 451

 N P A P G A Q Q M G P P Y Y T D P G G P 125
 AAT CCT GCT CCA GGA GCA CAG CAA ATG GGA CCG CCA TAT TAC ACC GAC CCT GGA GGA CCC 511

 G M N P V G N T M A M A F Q V Q P N S P 145
 GGG ATG AAT CCT GTT GGC AAT ACC ATG GCT ATG GCT TTC CAG GTC CAG CCC AAT TCA CCT 571

 H G G T T Y P P P S Y C N T P P P Y 165
 CAC GGA GGC ACA ACT TAC CCA CCC CCT CCT TCC TAC TGC AAC ACG CCT CCA CCC CCC TAT 631

 E Q V V K D K * 173
 GAA CAG GTG GTG AAG GAC AAG TAG 655

 CAAGATGCTACATCAAGGCAAGAGGATGGACAGGCCCTTTTGTACCTTCCCATCTCACCATACTTGCTGATAG 734

69 / 95

Fig. 4E

GGTGGTCCAAGGGAACCTTGGATAATTCTCAAAGCAAGCCAGCTCTCTTTCAAAGTCTTTTGTGGAGACATTGATC 813
CACACTGTCTCCTCTGTGTTCTGTCTGTCTCTGAGAGAGTGAGGCAACAGTCCCTGAGGGTT 892
GATATTCTAGGTGTCCAGGGTAGATCCTCGGGAGAGAGGCTAAGGGAAAGGCAAGCCTGTGTGTAGGGG 971
CAGATAAAGTGGTCAGGCTGAGATAAGACTCACATGATGCAGTAGTTGGCAGTGAACCTCGAAGAGACACTATCCACCA 1050
TCCAGCCCATTTCTCTAAATAGAAGCTGTGGGCTGTGTTGTGATGCTCTTTGGTCTCCACTCACATTTTGAAAAATAG 1129
GCTTTCTCTGCAGGAATAGGAAAGACCCCAAGTACATATTTGCTTCCACTTAAAAATGAGGGTCAGAACCCAGCCTCAG 1208
TTGGACATCTATAGTTAAATAAAGGCCATTAGAGAGGGGAAATCTTTAAGTTAGGGGAAATTCCTAAATGGAGACATT 1287
GCGTTTATGAATCATCGTCTGGCTTTTCTTTAGTGCAATGATTAAGTGAGGGTGCTCTTTGAGATCAGATGGGGAG 1366
AGTGAACTCTCGGGGGTGGGTGTCTCTACTCAGAGGGCTCCAAACCCCTTTTCTTAGGTAGTTCTGTTGATGGGTT 1445
TTATGGGCACTATAGAGCTGAGGGGCACATTAGGCCGGGTAGTTACATTTGACCCCTTGGAGAGGAAGAGGACAGCCAAAG 1524
AAACTCAGCAAAAGCAAGCAGCATTTGCTGAGTTAGAGCTAGGGTTGTATGTATGATCCCAACAGAGATGTGCTGGCCTCA 1603
GAAGAGGGACGTTTGTGGATAGAGCCGTGAACCTACTTAGTTGCACAGATGACATAATCAAAAGTAGAGAAAGAAAG 1682
TGTAGTTAGAGATGCCATTTCCCAGGTGAGAAATCAGAGCTCATCCATAGATTTACAAAGTAGTGGCTGGAGTTAACAGTA 1761
TGGAGTTCTTTCCCTTGGCTAGTTAGTCACGTTGATGTATTTAAACCCAGGTTGAGACCTTGTGTACTAAGAGCAA 1840
GGAAGTATAGCTAAGATGTCTAGATTTATATATGATGTTAGTGGGAGTGGGCTGCAAGGAAGGGGCTGACATTG 1919
TAAATGAGAAAAATCAGAGCCATTTGATAAATGTTACTTGTGGATCAGGCATCCAAAGTGCTCTCTTGAGTGGACATT 1998
GAGTATTTTACCACCTACAAGACCAGAGGCATGGTGTCATTTCTCCATTGGGGTATTTATATGAGGTAGAGGTTTCAG 2077
GAATCGACAGTAGCTGTGGCTTAGTTAAGGACTGAAAGCATAGGACTGGTAGACAGTTTCATAGGAAACTGCGG 2156
GGAAGGAATGGATACCTTTAAAGACAGTTTGTGGATGCAGATGCTGCCACCCCATCATTGAGCACCCCTTGTGCTCTGGC 2235
TTCCTGTCACTGGATCCAGTACCCCTCCATGCTTGGGTCCCTTGTTTTACATAAGACAAACAAAGCACAAATGTCTGTGTT 2314
TACAAATCAAGACGACTACATGGTCCAAAACATTTCTCTCTCTCTATCATTGTGGCTTTAACTTCCATTTCCTCCGTT 2393
CCTTTTAAAAATCAAGAAGCACAGTCAGAGCTGCCCTGGGATTGCATCAGGGAACGGCTGATCAAGGCATTCAGTGC 2472
CATGACTAAATCTTATCTTTTGTATAGCAAAATCCTTTTAAGAAACTGAACAAATTGCTAAGGCTCAGCAATTTTATACTC 2551
CAATGTCTGTGAAGGTAAATTTTGTGTTGCCATTGAGCCCCACATTTGGAATTCCTTCTGACGTCAACACTGACAAATGCT 2630
ATGGAAATTGCACTTCTGGGTATATGTCCCAGCATCCTTGTCTTATGTTTGGTGAGTAAGGCTCACCCCTTCCAGC 2709

Fig. 4F

AGCTCTACTTCTGTGCTGAGGTCCTGTAGAGCCGGGCTTGGCACACAGACATGAGGCAGACTTGTGCAATGCTCTTTC 2788
 TTGGCAACACTTGGCTCATATTTCTTCTCTTCTTTGATAGAGTCCTGTTCCTATGTATTTAAAAAATAATAAAAGTG 2867
 AATTAGTCAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 2915

Fig. 4G

	10	20	30	40	50	60	70
Hum.	MRRQPAKVAALLLGLLLECTEAKKHCHWYFEGLYPTYIICRSYEDCCGSRCCVRALS	IQRLWYFWFLMMG					
	:	:	:	:	:	:	:
Mur.	MGRRLGRVAALLLGLLVECTEAKKHCHWYFEGLYPTYIICRSYEDCCGSRCCVRALS	IQRLWYFWFLMMG					
	10	20	30	40	50	60	70
	80	90	100	110	120	130	140
Hum.	VLFCGAGFFIRRRMYPPPLIEEPAFNVSYTRQPNPGPGAQQPGPPYYTDGGPGMNPVGNSMAMAFQV						
	:	:	:	:	:	:	:
Mur.	VLFCGAGFFIRRRMYPPPLIEEPTFNVSYTRQPNPAPGAQQMGPPYYTDGGPGMNPVGNTMAMAFQV						
	80	90	100	110	120	130	140
	150	160	170				
Hum.	PPNSPQGSVACPPPPAYCNTPPPPYEQVVKAK						
	:	:	:	:	:	:	:
Mur.	QPNSPHGGTTYPPPPSYCNTPPPPYEQVVKDK						
	150	160	170				

Fig. 4H

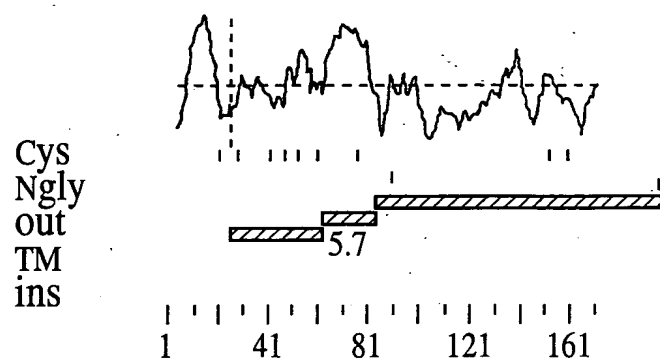


Fig. 4I

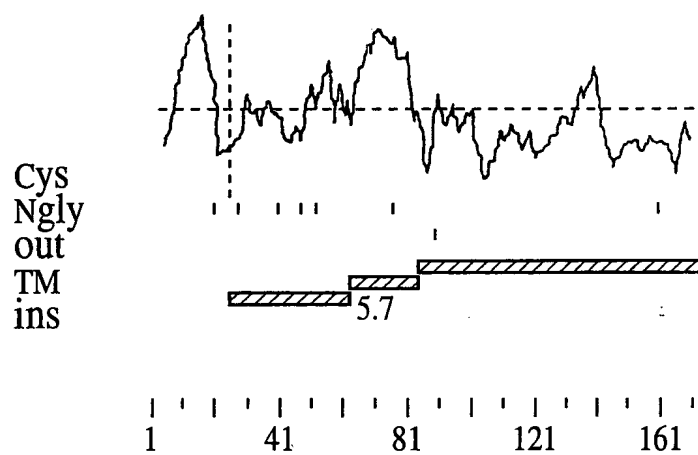


Fig. 4J

GTCGACCCACGCGTCCGACGCTTTGGACACTTCTGCTGCTTGAGGACACCTTGACTAACCTCCAAGGCAACTAAAGGA 79
 TCAAGAAAGGCCACAGCACAGCAAGATCAGCTGGATCTAGCTCCTGCAGGAG ATG TGT ACA AAG ACA ATC 150
 M C T K T I 6
 P V L W G C F L L L W N L Y V S S S Q T I 26
 CCA GTC CTC TGG GGA TGT TTC CTC CTG CTG TGG AAT CTC TAT GTC TCA TCC TCT CAG ACC ATT 210
 Y P G I K A R I T Q R A L D Y G V Q A G 46
 TAC CCT GGA ATC AAG GCA AGG ATT ACT CAG AGG GCA CTT GAC TAT GGT GGT CAA GCT GGA 270
 M K M I E Q M L L K E K K L P D L S G S E 66
 ATG AAG ATG ATT GAG CAA ATG CTA AAA GAA AAG AAA CTC CCA GAT TTA AGC GGT TCT GAG 330
 S L E F L K V D Y V N Y N F S N I K I S 86
 TCT CTT GAA TTT CTA AAA GTT GAT TAT GTA AAC TAC AAT TTT TCA AAT ATA AAA ATC AGT 390
 A F S F P N T S L A F V P G V G I K A L 106
 GCC TTT TCA TTT CCA AAT ACC TCA TTG GCT TTT GTG CCT GGA GTG GGA ATC AAA GCG CTA 450
 T N H G T A N I S T D W G F E S P L F V 126
 ACC AAC CAT GGC ACT GCC AAC ATC AGC ACA GAC TGG GGG TTC GAG TCT CCA CTT TTT GTT 510
 L Y N S F A E P M E K P I L K N L N E M 146
 CTG TAT AAC TCC TTT GCT GAG CCC ATG GAG AAA CCC ATT TTA AAG AAC TTA AAT GAA ATG 570

Fig. 5A

L C P I I A S E V K A L N A N L S T L E 166
 CTC TGT CCC ATT ATT GCA AGT GAA GTC AAA GCG CTA AAT GCC AAC CTC AGC ACA CTG GAG 630

 V L T K I D N Y T L L D Y S L I S S P E 186
 GTT TTA ACC AAG ATT GAC AAC TAC ACT CTG CTG GAT TAC TCC CTA ATC AGT TCT CCA GAA 690

 I T E N Y L D L N L K G V F Y P L E N L 206
 ATT ACT GAG AAC TAC CTT GAC CTG AAC TTG AAG GGT GTA TTC TAC CCA CTG GAA AAC CTC 750

 T D P P F S P V P F V L P E R S N S M L 226
 ACC GAC CCC TTC TCA CCA GTT CCT TTT GTG CTC CCA GAA CGC AGC AAC TCC ATG CTC 810

 Y I G I A E Y F F K S A S F A H F T A G 246
 TAC ATT GGA ATC GCC GAG TAT TTC TTT AAA TCT GCG TCC TTT GCT CAT TTC ACA GCT GGG 870

 V F N L T L S T E E I S N H F V Q N S Q 266
 GTT TTC AAT CTC ACT CTC TCC ACC GAA GAG ATT TCC AAC CAT TTT GTT CAA AAC TCT CAA 930

 G L G N V L S R I A E I Y I L S Q P F M 286
 GGC CTT GGC AAC GTG CTC TCC CGG ATT GCA GAG ATC TAC ATC TTG TCC CAG CCC TTC ATG 990

 V R I M A T E P P I I N L Q P G N F T L 306
 GTG AGG ATC ATG GCC ACA GAG CCT CCC ATA ATC AAT CTA CAA CCA GGC AAT TTC ACC CTG 1050

 D I P A S I M M L T Q P K N S T V E T I 326
 GAC ATC CCT GCC TCC ATC ATG ATG CTC ACC CAA CCC AAG AAC TCC ACA GTT GAA ACC ATC 1110

74 / 95

Fig. 5B

V S M D F V A S T S V G L V I L G Q R L 346
 GTT TCC ATG GAC TTC GTT GCT AGT ACC AGT GTT GGC CTG GTT ATT TTG GGA CAA AGA CTG 1170

 V C S L S L N R F R L A L P E S N R S N 366
 GTC TGC TCC TTG TCT CTG AAC AGA TTC CGC CTT GCT TTG CCA GAG TCC AAT CGC AGC AAC 1230

 I E V L R F E N I L S S I L H F G V L P 386
 ATT GAG GTC TTG AGG TTT GAA AAT ATT CTA TCG TCC ATT CTT CAC TTT GGA GTC CTC CCA 1290

 L A N A K L Q Q G F P L P N P H K F L F 406
 CTG GCC AAT GCA AAA TTG CAG CAA GGA TTT CCT CTG CCC AAT CCA CAC AAA TTC TTA TTC 1350

 V N S D I E V L E G F L L I S T D L K Y 426
 GTC AAT TCA GAT ATT GAA GTT CTT GAG GGT TTC CTT TTG ATT TCC ACC GAC CTG AAG TAT 1410

 E T S S K Q Q P S F H V W E G L N L I S 446
 GAA ACA TCC TCA AAG CAG CAG CCA AGT TTC CAC GTA TGG GAA GGT CTG AAC CTG ATA AGC 1470

 R Q W R G K S A P * 456
 AGA CAG TGG AGG GGG AAG TCA GCC CCT TGA 1500

 TTGCCGGTTTGCATTCACCCAGGAAGTAAATGGTCCTTAATCCTACAACACTACTGTAAACCCAGAAAGGAAAGACAGT 1579
 ACACACTGGAATTGTAAAGCCCTTGTGAATTGCTTAGGCAGAAAGTTTCTTTAAGCCTTCAGGAACCCAGAAATAA 1658
 GGCAGACTCTGTTAAAGGGATAAATAGAGGTGTCTGAATGTGAGTGATGCATGCTGCGTGTCTGTTTATGTTG 1737
 TTTGTTTGTGGGCAAGAAAGATTCTAGGACAAGAGCTAGGCATGTACTTCTGACCAGGTGGGTAAAGCAACTCTAAG 1816

75 / 95

Fig. 5C

TCTGTAATTGTCATTCTCAGTGGAAATCCCTTAGGCCCTCTAGTGGTTTTCCTACCTGCATAATTGGTTTC 1895
ATGTTTTATATTCACCTGTTACTATCTTCTGTGTTTAAATTAAATTTCTATCAAAAAAAAAAAAAAAAAAGGGC 1974
GGCCGC 1980

Fig. 5D

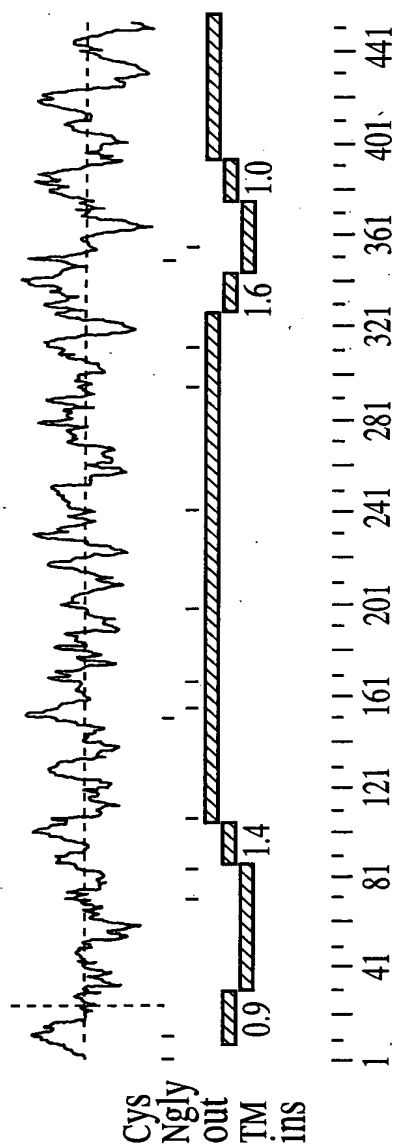


Fig. 5E

```

10      20      30      40      50      60
286 MCTKT-IPVLWGCFL-LWNLVSSSQTIYPGIKARITQRALDYGVAQGMKMIQMLKEKKLPDLGSESL
:      :      :      :      :      :      :      :      :      :      :
BPI MARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS--DSF
10      20      30      40      50      60

70      80      90      100     110     120     130
286 EFLKVDYVNYNFSNIKISAFSEFPNTSLAFVPGVGIKALTNHGTANISTDWGFESPLFVLVNSFAEPM---
:      :      :      :      :      :      :      :      :      :      :
BPI KIKHLGKGHSFYSDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKMSGNFDLSIEGM
70      80      90      100     110     120     130

286 -----KPI-----140     150
:      :      :      :      :      :      :      :      :      :      :
BPI SISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSVGWLIQLFHKKIESALRNKMNSQVCEKVTNS
140     150     160     170     180     190     200

286 VKA-LNANLSTLEVLTKIDNYTLDDYSLISSPEITENYLDNLKGVFYPLENLTDPFPSPVFPVLPERSN
:      :      :      :      :      :      :      :      :      :      :
BPI VSSKLQPYFQTLPVMTKIDSVAGINYGVLVAPPATTAETLDVQMKGEFYSENHHNPPFPFAPPVMEFFPAAHD
210     220     230     240     250     260     270

```

Fig. 5F

230	240	250	260	270	280	290
286	SMLYIGIAEYFFKSAFAHFTAGVFNLTLS	TEEISNH--FVQNSQGLGNVLSRIA	EIYILSQPFMVRIMA			
BPI	RMVYGLSDYFFNTAGLVYQ	EAGVLKMTLRDDMIPKESK	FRLTTKFFGTFLPEVAKKFP-NMKIQIHVSA			
280	290	300	310	320	330	340
286	TEPPIINLQPGNFTLDIPASIMMLTQPKNSTVETIVSMDFVASTVGLVILGQRLVCSLSLNRFR	LALPE				
BPI	STPPHLSVQPTGLTFYP	PAVDVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNR	LVGELKLDRLLELKH			
350	360	370	380	390	400	410
286	SNRSNIEVLRFENILSSILHFGVLPLANAKLQQGFPLPNPHKFLFVN	SDIEVLEGFLLISTDLKYETSSK				
BPI	SNIGPFPVELLQDIMN	YIVPILVLRVNEKLQKGFPLPTPARVQLYNVVLQPHQNFL	FGADVYK----			
420	430	440	450	460	470	480
286	QQPSFHVWEGNLISRQWRGKSAP					
BPI	-----					

1882

File 5H

Fi. 5

GTCGACCCACGCGTCCGGGAAATTGCAGCAGGAAATAATGTGAAGAGTTTTTAAACCCACAAAATTCTTCTTACTTTAGA	79
<div style="text-align: center;"> M L E T L S R Q </div>	
ATTAGTTGTACATTGGCAGGAAAAATAAATGCAGATGTTGGACC ATG TTG GAA ACC TTG TCA AGA CAG	149
W I V S H R M E M W L L I L V A Y M F Q	28
TGG ATT GTC TCA CAC AGA ATG GAA ATG TGG CTT CTG ATT CTG GTG GCG TAT ATG TTC CAG	209
R N V N S V H M P T K A V D P E A F M N	48
AGA AAT GTG AAT TCA GTA CAT ATG CCA ACT AAA GCT GTG GAC CCA GAA GCA TTC ATG AAT	269
I S E I I Q H Q G Y P C E E Y E V A T E	68
ATT AGT GAA ATC ATC CAA CAT CAA GGC TAT CCC TGT GAG GAA TAT GAA GTC GCA ACT GAA	329
D G Y I L S V N R I P R G L V Q P K K T	88
GAT GGG TAT ATC CTT TCT GTT AAC AGG ATT CCT CGA GGC CTA GTG CAA CCT AAG AAG ACA	389
G S R P V V L L Q H G L V G G A S N W I	108
GGT TCC AGG CCT GTG GTG TTA CTG CAG CAT GGC CTA GTT GGA GGT GCT AGC AAC TGG ATT	449
S N L P N N S L G F I L A D A G F D V W	128
TCC AAC CTG CCC AAC AAT AGC CTG GGC TTC ATT CTG GCA GAT GCT GGT TTT GAC GTG TGG	509
M G N S R G N A W S R K H K T L S I D Q	148
ATG GGG AAC AGC AGG GGA AAC GCC TGG TCT CGA AAA CAC AAG ACA CTC TCC ATA GAC CAA	569

Fig. 6A

D E F W A F S Y D E M A R F D L P A V I 168
GAT GAG TTC TGG GCT TTC AGT TAT GAT GAT GAG ATG GCT AGG TTT GAC CTT CCT GCA GTG ATA 629
N F I L Q K T G Q E K I Y Y V G Y S Q G 188
AAC TTT ATT TTG CAG AAA ACG GGC CAG GAA AAG ATC TAT TAT GTC GGC TAT TCA CAG GGC 689
T T M G F I A F S T M P E L A Q K I K M 208
ACC ACC ATG GGC TTT ATT GCA TTT TCC ACC ATG CCA GAG CTG GCT CAG AAA ATC AAA ATG 749
Y F A L A P I A T V K H A K S P G T K F 228
TAT TTT GCT TTA GCA CCC ATA GCC ACT GTT AAG CAT GCA AAA AGC CCC GGG ACC AAA TTT 809
L L L P D M M I K G L F G K K E F L Y Q 248
TTG TTG CTG CCA GAT ATG ATG ATC AAG GGA TTG TTT GGC AAA AAA GAA TTT CTG TAT CAG 869
T R F L R Q L V I Y L C G Q V I L D Q I 268
ACC AGA TTT CTC AGA CAA CTT GTT ATT TAC CTT TGT GGC CAG GTG ATT CTT GAT CAG ATT 929
C S N I M L L L G G F N T N N M N M S R 288
TGT AGT AAT ATC ATG TTA CTT CTG GGT GGA TTC AAC ACC AAC AAT ATG AAC ATG AGC CGA 989
A S V Y A A H T L A G T S V Q N I L H W 308
GCA AGT GTA TAT GCT GCC CAC ACT CTT GCT GGA ACA TCT GTG CAA AAT ATT CTA CAC TGG 1049
S Q A V N S G E L R A F D W G S E T K N 328
AGC CAG GCA GTG AAT TCT GGT GAA CTC CGG GCA TTT GAC TGG GGC AGT GAG ACC AAA AAT 1109

Fig. 6B

L E K C N Q P T P V R Y R V R D M T V P 348
 CTG GAA AAA TGC AAT CAG CCA ACT CCT GTA AGG TAC AGA GTC AGA GAT ATG ACG GTC CCT 1169
 T A M W T G G Q D W L S N P E D V K M L 368
 ACA GCA ATG TGG ACA GGA GGT CAG GAC TGG CTT TCA AAT CCA GAA GAC GTG AAA ATG CTG 1229
 L S E V T N L I Y H K N I P E W A H V D 388
 CTC TCT GAG GTG ACC AAC CTC ATC TAC CAT AAG AAT ATT CCT GAA TGG GCT CAC GTG GAT 1289
 F I W G L D A P H R M Y N E I I H L M Q 408
 TTC ATC TGG GGT TTG GAT GCT CCT CAC CGT ATG TAC AAT GAA ATC ATC CAT CTG ATG CAG 1349
 Q E E T N L S Q G R C E A V L * 424
 CAG GAG GAG ACC AAC CTT TCC CAG GGA CGG TGT GAG GCC GTA TTG TGA 1397
 AGCATCTGACACTGACGATCTTAGGACAACTCCTGAGGGATGGGGCTAGGACCCCATGAAGGCCAGAAATTACGGAGAGCA 1476
 GAGACCTAGTATACATTTTTCAGATTCCCTGCACCTTGGCACTAAATCCGACACTTACATTTTCTGTAAA 1555
 TTAAGTACTTATTAGGTAAATAGAGGTTTGTATGCTATTATATATCTACCATCTTGAAGGTAGGTTTACCTGAT 1634
 AGCCAGAAAATATCTAGACATTCTCTATATCATTCAGGTAAATCTCTTTAAACACCATTTGTTTTCTATAGAAGCCAT 1713
 ATTTTGGAGCACTAAAGTAAATGGCAAAATGGGACAGATATTGAGGTCTGGAGTCTGTGGATTATTGTTGACTTTGA 1792
 CAAAATAAGCTAGACATTTTCACCTTGTGTCACAGACATAACACTACCTCAGGAAGCTGAGCTGCTTAAAGGACAA 1871
 CAACAACAAAATCAGTGTACAGTATGGATGAAATCTATGTTAAGCATTTCTCAGAAATAAGGCCAAGTTTATAGTTGCA 1950
 TCTCAGGGAAGAAAATTTTATAGGATGTTTATGAGTTCTCCAATAAATGCATTCTGCATTACATAAAAAA 2029
 AAAAAAGGCGGCGCGC 2044

Fig. 6C

```

10      20      30      40      50      60      70
294 MLETLRQWIVSHRMEMWLLILVAYMFQRVNNSVHMPTKAVDPEAFMNISEIIQHGYPCEEYEVEDG
:      :      :      :      :      :      :
HLP M-----WLL-----LTMASLISVLGTTGHLFGKLH-----PGSPEVTMNISQMITYWGYPNEEYEVVTE
10      20      30      40      50
294 YILSVNRIPRGLVQPKKTGSRPVVLLQHLVGGSNWNISLNPNSLGFILADAGFDVWMGNSRGNWSRK
:      :      :      :      :      :      :
HLP YILEVNRIPYGKKNSGNTGQRPVFLQHGLLASATNWNISLNPNSLAFILADAGYDVWLGNRGNWTWARR
60      70      80      90      100      110      120
294 HKTLSIDQDEFWAFSYDEMAREFDLPVAVINFILQKTGQEKIYYVGYSGTGMGFIAFSTMPELAQIKMYF
.      :      :      :      :      :      :
HLP NLYYSPDSVEFWAFSFDDEMAKYDLPATIDFIVKKTGQKQLHYVGHSGQTTIGFIAFSTNPSLAKRIKTFY
130      140      150      160      170      180      190
294 ALAPIATVKHAKSPGTKFLLLPDMMIKGLFGKKEFLYQTRFLRQ-LVIYLCGQVILDQICSNIMLLLGGF
:      :      :      :      :      :      :
HLP ALAPVATVKYTKSLINKLRFVPQSLFKFIFGDKIF-YPHNFFDQFLATEVCSREMLNLLCSNALFIICGF
200      210      220      230      240      250      260

```

Fig. 6D

```

280      290      300      310      320      330      340
294 NTNNMMSRASVYAAHTLAGTSVQNIHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRYRVRDMTVPT
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
HLP DSKNFNTSRDLVDYLSHNPAGTSVQNMFWHTQAVKSGKFOAYDWGSPVQNRMHYDQSQPPYYNVVTAMNVPI
    270      280      290      300      310      320      330

350      360      370      380      390      400      410
294 AMWTGGQDWLSNPEDVKMILLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNEIIHLMQQEETNLSQGR
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
HLP AVWNGGKDLLADPPQDVGLLPKLPNLIYHKEIPFYNHLDFIWAMDAPQEVYNDIVSMISEDKK-----
    340      350      360      370      380      390

```

420

294 EAVL

HLP ----

Fig. 6E

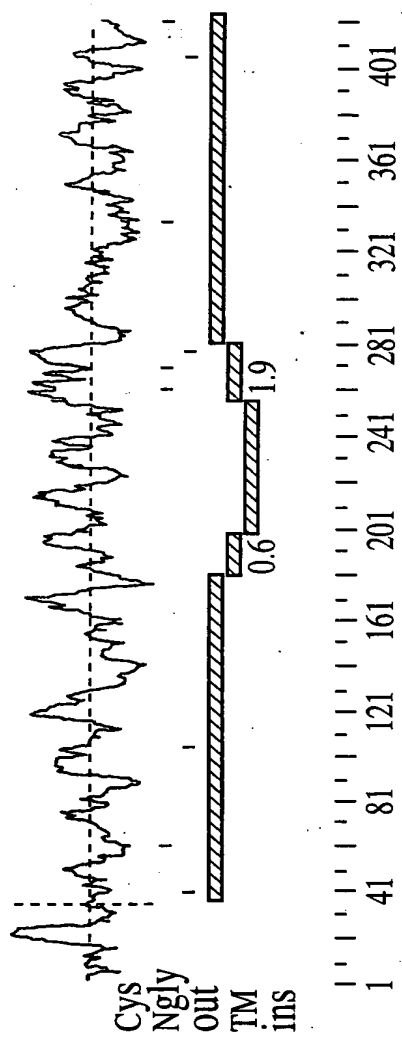


Fig. 6F

```

10      20      30      40      50      60
294 MLETLRQWIVSHRMEMWLLILVAYMFQRNVNSVHMPK--AVDPEAFMNISEIIQHQQYPCPEEYEVATE
      :      :... :... :      :      :      :      :      :      :      :
      :      :... :... :      :      :      :      :      :      :      :
LAL M-----KMRFLGLVVCLVWPLHSEGSCKLTAVDPETNMNVSEIISYWGFPSSEYLVETE
      10      20      30      40      50

70      80      90      100      110      120      130
294 DGYILSVNRIPRGLVQPKKTGSRPVVLLQHGLVGGASNWNLPNNSLGFILADAGFDVWMGNSRGNWS
      :      :      :      :      :      :      :      :      :      :      :
      :      :      :      :      :      :      :      :      :      :      :
LAL DGYILCLNRI PHGRKNHSDKGPVVFLOHGLLADSSNWWVTNLANSSLGFILADAGFDVWMGNSRGNTWS
      60      70      80      90      100      110      120

140     150     160     170     180     190     200
294 RKHKTLSDQDEFWAFSYDEMAREFDLPAVINFILQKTGQEKIYYVGYSGQTTMGFIAFSTMPELAQIKM
      :      :      :      :      :      :      :      :      :      :      :
      :      :      :      :      :      :      :      :      :      :      :
LAL RKHKTLVSQDEFWAFSYDEMAYDLPASINFILNKTGQEQVYVVGHSQGTIGFIAFSQIPELAKRIKM
      130     140     150     160     170     180     190

210     220     230     240     250     260     270
294 YFALAPIATVVKHAKSPGTKFLLLPDMMIKGLFGKKEFLYQTRFLRQLVIYLCGQVILDQICSNIMLLGG
      :      :      :      :      :      :      :      :      :      :      :
      :      :      :      :      :      :      :      :      :      :      :
LAL FFALGPVASVAFCTSPMAKLGRLPDHLIKDLFGDKFELPQSAFLKWLGTHVCTHVLKELCGNLCFLLCG
      200     210     220     230     240     250     260

```

Fig. 6G

280 290 300 310 320 330 340
294 FNTNNMMSRASVYAAHTLAGTSVQNILHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRVVRDMTVP
:: :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
LAL FNERNLNMSRVDVYTTHTSPAGTSVQNMLHWSQAVKFKQFAFDWGSSAKNYFHYNQSYPPPTYNVKDMMLVP
270 280 290 300 310 320 330
350 360 370 380 390 400 410
294 TAMWTGGQDWLSNPEDVKMLLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNEIIHLMQQEETNLSQGR
:::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
LAL TAVWSGGHDWLADVVDVNILLTQITNLVFHESIPWEHLDFIWGLDAPWRLYNKIIINLMRKYQ-----
340 350 360 370 380 390

420

294 CEAVL

LAL -----

Fig. 6H

GTCGACCCACGCGTCCACGGCGGAGGGCTCCCGGGCGGAGCATTCGCCCCCTGCACCACTCACCAG ATG GCT 75

T L G H T F P F Y A G P K P T F P M D T 22
ACT TTG GGA CAC ACA TTC CCC TTC TAT GCT GGC CCC AAG CCA ACC TTC CCG ATG GAC ACC 135

T L A S I I M I F L T A L A T F I V I L 42
ACT TTG GCC AGC ATC ATC ATG ATC TTT CTG ACT GCA CTG GCC ACG TTC ATC GTC ATC CTG 195

P G I R G K T R L L F W L L R V V T S L F 62
CCT GGC ATT CGG GGA AAG ACG AGG CTG TTC TGG CTG CTT CGG GTG GTG ACC AGC TTA TTC 255

I G A A I L A V N F S S E W S V G Q V S 82
ATC GGG GCT GCA ATC CTG GCT GTG AAT TTC AGT TCT GAG TGG TCT GTG GGC CAG GTC AGC 315

T N T S Y K A F S S E W I S A D I G L Q 102
ACC AAC ACA TCA TAC AAG GCC TTC AGT TCT GAG TGG ATC AGC GCT GAT ATT GGG CTG CAG 375

V G L G G V N I T L T G T P V Q Q L N E 122
GTC GGG CTG GGT GGA GTC AAC ATC ACA CTC ACA GGG ACC CCC GTG CAG CAG CTG AAT GAG 435

T I N Y N E E F T W R L G E N Y A E E C 142
ACC ATC AAT TAC AAC GAG GAG TTC ACC TGG CGC CTG GGT GAG AAC TAT GCT GAG GAG TGT 495

A K A L E K G L P D P V L Y L A E K F T 162
GCA AAG GCT CTG GAG AAG GGG CTG CCA GAC CCT GTG TTG TAC CTA GCT GAG AAG TTC ACT 555

Fig. 7A

P	R	S	P	C	G	L	Y	R	Q	Y	R	L	A	G	H	Y	T	S	A	182
CCA	AGA	AGC	CCA	TGT	GGC	CTA	TAC	CGC	CAG	TAC	CGC	CTG	GCG	GGA	CAC	TAC	ACC	TCA	GCC	615
M	L	W	V	A	F	L	C	W	L	L	A	N	V	M	L	S	M	P	V	202
ATG	CTA	TGG	GTG	GCA	TTC	CTC	TGC	TGG	CTG	CTG	GCC	AAT	GTG	ATG	CTC	TCC	ATG	CCT	GTG	675
L	V	Y	G	G	Y	M	L	L	A	T	G	I	F	Q	L	L	A	L	L	222
CTG	GTA	TAT	GGT	GGC	TAC	ATG	CTA	TTG	GCC	ACG	GGC	ATC	TTC	CAG	CTG	TTG	GCT	CTG	CTC	735
F	F	S	M	A	T	S	L	T	S	P	C	P	L	H	L	G	A	S	V	242
TTC	TTC	TCC	ATG	GCC	ACA	TCA	CTC	ACC	TCA	CCC	TGT	CCC	CTG	CAC	CTG	GGC	GCT	TCT	GTG	795
L	H	T	H	H	G	P	A	F	W	I	T	L	T	T	G	L	L	C	V	262
CTG	CAT	ACT	CAC	CAT	GGG	CCT	GCC	TTC	TGG	ATC	ACA	TTG	ACC	ACA	GGA	CTG	CTG	TGT	GTG	855
L	L	G	L	A	M	A	V	A	H	R	M	Q	P	H	R	L	K	A	F	282
CTG	CTG	GGC	CTG	GCT	ATG	GCG	GTG	GCC	CAC	AGG	ATG	CAG	CCT	CAC	AGG	CTG	AAG	GCT	TTC	915
F	N	Q	S	V	D	E	D	P	M	L	E	W	S	P	E	E	G	G	L	302
TTC	AAC	CAG	AGT	GTG	GAT	GAA	GAC	CCC	ATG	CTG	GAG	TGG	AGT	CCT	GAG	GAA	GGT	GGA	CTC	975
L	S	P	R	Y	R	S	M	A	D	S	P	K	S	Q	D	I	P	L	S	322
CTG	AGC	CCC	CGC	TAC	CGG	TCC	ATG	GCT	GAC	AGT	CCC	AAG	TCC	CAG	GAC	ATT	CCC	CTG	TCA	1035
E	A	S	S	T	K	A	Y	C	K	E	A	H	P	K	D	P	D	C	A	342
GAG	GCT	TCC	TCC	ACC	AAG	GCA	TAC	TGT	AAG	GAG	GCA	CAC	CCC	AAA	GAT	CCT	GAT	TGT	GCT	1095

Fig. 7B

L * 344
 TTA TAA 1101

CATTCCTCCCGTGGAGGCCACCTGGACTTCCAGTCTGGCTCCAAACCTCAATTGGCGCCCCATAAAACCAGCAGAACTG 1180
 CCTCAGGGTGGCTGTTACCAAGACACCCAGCACCAATCTACAGACGGAGTAGAAAAAGGAGGCTCTATATACTGATGTT 1259
 AAAAAACAAAAACAAAAAGCCCTAAGGACTGAAGAGATGCTGGGCTGTCCATAAAGCCCTGTTGCCATGATAAG 1338
 GCCAAGCAGGGCTAGCTTATCTGCACAGCAACCCAGCCTTCCGTGCTGCCCTTCCCTCTTCAAGATGCTATTCACTGA 1417
 AACCTAACTTCACCCCATAAACACAGCAGGGTGGGGTTACATAATGATTCTCCTATGGTTTCCCTCTCATCCCTCGGCA 1496
 CCTCTTGTTTTTCCCTGGGTTCCCTTTTGTTCTTCCCTTACTTCTCCAGCTTGTGTGGCCTTTTGGTACAATGAA 1575
 AGACAGCACTGGAAGGAGGGAACCAACTTCTCATCCTAGGTCTAACATTAAACCAACTATGCCACATTCCTTTGA 1654
 GCTTCAGTTCCTCCAAATTTGCTACATAAGATTGCAAGACTTGCCAAGAACTTTGGGATTTATCTTCTATGCCCTTGCTGA 1733
 CACCTACCTTGGCCCTCAAAACACCCCTCACAAGAAGCCAGGTGGGAAGTTAGGGAATCAACTCCAAAAACGCTATTCTT 1812
 TCCACCCCACTCAGCTGGCTAGCTGAGTGGCATCCAGGACGGGGAGTGGTGACCTGCCTCATCACTGCCACCTAA 1891
 CGTCCCTCCCTGGGTGTTCAGAAAGATGCTAGCTCTGTAGGTCCCTCCGGCTCACTAGAGGGCGCCCTATTACTC 1970
 TGGAGTCGACGCAGAGAAATCAGGTTTTCACAGCACTGCCGGAGAGTGTAAGGTGTCTCCAGCCAGCGAAGCTCATGA 2049
 GGACGTGCGACCCCGCGGAGAGCCATGAAAAATTAATGGGAAAAAACAGTTTTTAAAAAAGGGGGG 2128
 GCCGC 2133

92 / 95

Fig. 7C

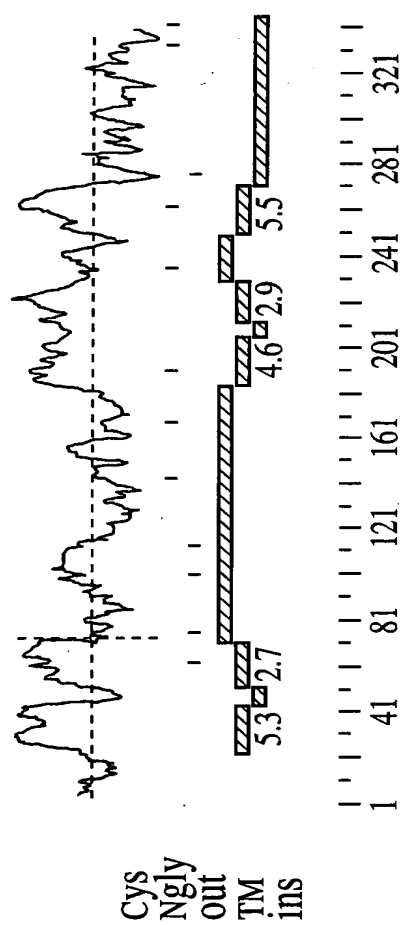


Fig. 7D

```

10      20      30      40      50      60      70
296 MATLGHTFPFYAGPKPTFPMDTTLASIIMIFLTALATFIVILPGIRGKTRLFWLLRVVTSLFIGAAILAV
:  ::  :...  :  :  :...  :  :  :...  :  :  :...  :  :  :...  :
CRP M-RIAH-----ASSRGN-----SIFSVFLIPLIAYILILPGVR-RKRVVTTVTYVLMMLAVGGALIAS
10      20      30      40      50

296 NFSSEWSVGQVSTNTSYKAFSESSEWISADIGLQVGLGVNITL-----TGPVQQQLNETIN--YNEEFTW
:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
CRP LIYPCWASGSQMIYTQFRGHSNERILAKIGVEIGLQKVNVTLKFERLLSSNDVLPGSDMTELYYNEGEDI
60      70      80      90      100      110      120

140      150      160      170      180      190      200
296 RIGENYAECAKALEKGLDPVLYLAEKFT-PRSPCGLYRQYRLAGHYTSAMLWVAFLCWLLIANV-MLSM
:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
CRP SGISSMAEALHHGLENGLPYPMLSVLEYFSLNQDSFDWGRHYRVAGHYTHAAIWFAFACWCCLSVVLMFL
130      140      150      160      170      180      190

210      220      230      240      250      260
296 PVLVYGGYMLLATGIFQLLALLFFSMATSLTSPCPLHL---GASVLTHHHGPAF---WITLTGLLCVL
:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
CRP PHNAYKS--ILATGISCLIACLVYL----LLSPCELRIAFGTGENFERVDLTATFSFCFYLI FAIGILCVL
200      210      220      230      240      250      260

```

Fig. 7E

```

270      280      290      300      310      320
296 IGLAMAVAHRMQPHRLKAFNQSVDEDEPMLEW-----SPEEGGLISPRY--RSMADSPKSQDIPLSEAS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CRP CGLGLGICEHWRIYTLSTFLDASLDEHVGPWKKLPTGGPALQGVQIGAYGTNTTNSRRDKNDISSDKTA
      270      280      290      300      310      320      330

      330
296 STKAY-----CK-----EAHPKDPD-----CA---L
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CRP GSSGFQSRSTCQSSASSASLRSQSSIETVHDEAELEERTHVHFLQEPCCSSST
      340      350      360      370      380

```

Fig. 7F